

GenCore version 5.1.6
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OM protein - nucleic search, using frame_plus_p2n model

Run on: August 18, 2004, 04:49:17 ; Search time 1365 Seconds
(without alignments)
5133.066 Million cell updates/sec

Title: US-10-020-095-4

Perfect score: 7348

Sequence: 1 MQGPPLTAHLLCVCTAAL.....HSSVIFPFCXLLYFMEMLWL 1428

Scoring table:

BLOSUM62
Xgapcp 10.0, Xgapext 0.5
Ygapcp 10.0, Ygapext 0.5
Fgapcp 6.0, Fgapext 7.0
Delop 6.0, Delext 7.0

Searched: 3225727 seqs, 2453303834 residues

Total number of hits satisfying chosen parameters: 6451454

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Command line parameters:

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-DB=Published Applications NA -QWTF=fastap -SUFFIX=p2n.rnpb -MINMATCH=0.1
-LOOPEXT=0 -UNLUS=bits -START=1 -END=1 -MATRIX=blosum62
-TRANS=human40.cdi -LIST=45 -DOCALIGN=200 -THR SCORE=pct -THR MAX=100
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-MAXLEN=2000000000 -USER=US10020095.@CGN_1.1_984 @runat_10082004_154042_17445
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-LONGLOG -DEV TIMEOUT=120 -WARN TIMEOUT=30 -THREADS=1 -XGAPOP=10 -XGAPEXT=0.5
-FCGAPOP=6 -FCGAPEXT=7 -YGAPOP=10 -YGAPEXT=0.5 -DELOP=6 -DELEXT=7

Database : Published Applications NA:

- 1: /cgn2_6/prodata/1/pubpna/US07_PUBCOMB.seq:
- 2: /cgn2_6/prodata/1/pubpna/PCT_NEW_PUB.seq:
- 3: /cgn2_6/prodata/1/pubpna/US06_PUBCOMB.seq:
- 4: /cgn2_6/prodata/1/pubpna/US06_PUBCOMB.seq:
- 5: /cgn2_6/prodata/1/pubpna/US07_NEW_PUB.seq:
- 6: /cgn2_6/prodata/1/pubpna/PCTUS_PUBCOMB.seq:
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- 8: /cgn2_6/prodata/1/pubpna/US08_PUBCOMB.seq:
- 9: /cgn2_6/prodata/1/pubpna/US09A_PUBCOMB.seq:
- 10: /cgn2_6/prodata/1/pubpna/US09B_PUBCOMB.seq:
- 11: /cgn2_6/prodata/1/pubpna/US09C_PUBCOMB.seq:
- 12: /cgn2_6/prodata/1/pubpna/US03_NEW_PUB.seq:
- 13: /cgn2_6/prodata/1/pubpna/US05_NEW_PUB.seq:
- 14: /cgn2_6/prodata/1/pubpna/US10A_PUBCOMB.seq:
- 15: /cgn2_6/prodata/1/pubpna/US10B_PUBCOMB.seq:
- 16: /cgn2_6/prodata/1/pubpna/US10C_PUBCOMB.seq:
- 17: /cgn2_6/prodata/1/pubpna/US10_NEW_PUB.seq:
- 18: /cgn2_6/prodata/1/pubpna/US60_NEW_PUB.seq:
- 19: /cgn2_6/prodata/1/pubpna/US60_PUBCOMB.seq:

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match Length	ID	Description
1	3033	0	4535.50	Length: 3033 Matches: 880

ALIGNMENTS

RESULT 1

US-09-833-381-1810
; Sequence 1810, Application US/09833381
; Patent No. US20020132090A1
; GENERAL INFORMATION:
; APPLICANT: Robison, Keith E.
; TITLE OF INVENTION: No. US20020132090A1el Nucleic Acid and Protein Homologs
; FILE REFERENCE: 5800-119
; CURRENT APPLICATION NUMBER: US/09/833.381
; CURRENT FILING DATE: 2001-04-11
; PRIOR APPLICATION NUMBER: 09/516,448
; PRIOR FILING DATE: 2000-02-29
; NUMBER OF SEQ ID NOS: 2050
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 1810
; LENGTH: 3033
; TYPE: DNA
; ORGANISM: Homo sapiens
US-09-833-381-1810

Alignment Scores:
Pred. No.: 0
Score: 4535.50
Length: 3033
Matches: 880

Percent Similarity:	98.00%	Conservative:	2	
Best Local Similarity:	97.78%	Mismatches:	1	
Query Match:	61.72%	Indels:	17	
DB:	9	Gaps:	1	
US-10-020-095-4 (1-1428) x US-09-833-381-1810 (1-3033)				
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Db	6	GTCCGAAAATTTCTGTTTCTGAGCTGTTTTTAAATAAAGTAAGTATATTGAGTAA 65		
Qy	566	ValLysAlaGluProSerGluLysValSerLeuArgIleSerValThrGlnProAspSer	585	ProAsnThrValThrGlySerGluArgValGlnIleThrAlaIleGlyAspValLeuGly 905
Db	66	GTCAAGAGCTGAACCATCTGAGAAAGTCTCTCTTAGGATCTCTGTGACACAGCGCTGACTCC 125		
Qy	586	IleValGlyIleValAlaValAspLysSerValAsnLeuMetAsnAlaSerAsnAspIle	605	MetIleAsnPheAlaProAsnIleTyIleLeuAspTyLeuThrLysLysLysGlnLeu 945
Db	126	ATAGTTGGGATTGTAGCTGTGTGACAAAGGTGAAATCTGATGAATGCCCTTAATGATATT 185		
Qy	606	ThrMetGluAsnValValHisGluLeuGluLeuTyAsnThrGlyTyTrpLeuGlyMet	625	ThrAspAsnLeuLysGluLysAlaLeuSerPheMetArgGlnGlyTyTrpGlnArgGluLeu 965
Db	186	ACAATGGAATTTGGTCCATGAGTTGGAACCTTATAACACAGCATATTATTAGGCATG 245		
Qy	626	PheMetAsnSerPheAlaValPheGlnGluCysGlyLeuTyTrpValLeuThrAspAlaAsn	645	LeuTyTrpGlnArgGluAspGlySerPheSerAlaPheGlyAsnTyTrpAspProSerGlySer 985
Db	246	TTCATGAATTTCTTTTGCAGTCTTTTCAGGAATGTGGACTCTGGGTATTGACAGATGCAAAAC 305		
Qy	646	LeuThrLysAspTyIleAspGlyValTyAspAsnAlaGluTyTrpAlaGluArgPheMet	665	CTCTATCAGAGGGAAGATGGCTCTTTTCAGTGTCTTTTGGGAATTTATGACCTTCTGGGAGC 1325
Db	306	CTACGAAAGATATTATTGATGTGTATTATGACATGCAGATATGCTGAGAGTTTATG 365		
Qy	666	GluGluAsnGluGlyHisIleValAspIleHisAspPheSerLeuGlySerSerProHis	685	ThrTrpLeuSerAlaPheValLeuArgCysPheLeuGluAlaAspProTyTrpIleAspIle 1005
Db	366	GAGGAAATGAAGCACATATTATGATATTATCATGACTTTCTTTGGGTAGCAGTCCACAT 425		
Qy	686	ValArgLysIshPheProGluThrTrpIleTrpLeuAspThrAsnMetGlyTyArgIle	705	CTCTATCAGAGGGAAGATGGCTCTTTTCAGTGTCTTTTGGGAATTTATGACCTTCTGGGAGC 1325
Db	426	GTCCGAAAGCATTTTCCAGAGACTTGGATTGGCTAGACACCAACATGGGTACAGATT 485		
Qy	706	TyrGlnGluPheGluValThrValProAspSerIleThrSerTrpValAlaThrGlyPhe	725	ValThrLeuThrAlaTyTrpIleValThrSerLeuLeuGlyTyArgLysTyTrpGlnProAsn 1065
Db	486	TACCAAGATTTGAAGTAACCTGATCTTATCATCTTTGGTGGCTACTGCTGTTT 545		
Qy	726	ValIleSerGluAspLeuGlyLeuGlyLeuThrThrProValGluLeuGlnAlaPhe	745	1506 GTAACACTTACAGCCTATATTGTAACCTTCTCTCTGGGATATAGAAAGTATCAGCCTAAC 1565
Db	546	GTGATCTCTCAGGACCTGGGTCTGGACTAACACTACTCCAGTGGAGTCCAAAGCCTTC 605		
Qy	746	GlnProPhePheIlePheLeuAsnLeuProTyTrpSerValIleArgGlyGluGluPheAla	765	1506 GTAACACTTACAGCCTATATTGTAACCTTCTCTCTGGGATATAGAAAGTATCAGCCTAAC 1565
Db	606	CAACCATTTTTCATTTTGTGAAATCTTCCCTACTCTGTTATCAGAGGTGAAGATTGCT 665		
Qy	766	LeuGluIleThrIlePheAsnTyTrpLeuLysAlaThrGluValLysValIleIleGlu	785	1106 GluAlaLeuAsnMetLeuThrTrpArgAlaGluGlnGlyMetGlnPheTrpVal 1125
Db	666	TTGAAATAAATATATTCAATTTATTGAAAGATGCCACTGAGGTAAAGTAAATCATTTAG 725		
Qy	786	LysSerAspLysPheAspIleLeuMetThrSerSerGluIleAsnAlaThrGlyHisGln	805	1106 GluAlaLeuAsnMetLeuThrTrpArgAlaGluGlnGlyMetGlnPheTrpVal 1125
Db	726	AAAAGTGACAAATTTGATTTCTAATGACTTCAATGAAATGAATGAATGCCACAGCCAC 785		
Qy	806	GlnThrLeuLeuValProSerGluAspGlyAlaThrValLeuPheProIleArgProThr	825	1106 GluAlaLeuAsnMetLeuThrTrpArgAlaGluGlnGlyMetGlnPheTrpVal 1125
Db	786	CAGACCTTCTGGTTCCTCAGTGGAGTGGGCAACTGTTCTTTTCCCATCAGGCCAACCA 845		
Qy	826	HisLeuGlyGluIleProIleThrValThrAlaLeuSerProThrAlaSerAspAlaVal	845	1106 GluAlaLeuAsnMetLeuThrTrpArgAlaGluGlnGlyMetGlnPheTrpVal 1125
Db	846	CATCTGGGAAATTTCTATCAGAGTACAGCTCTTTTCCACCACTCTTCTGATGATC 905		
Qy	846	ThrGlnMetIleLeuValLysAlaGluGlyIleGluLysSerTyTrpSerGlnSerIleLeu	865	1106 GluAlaLeuAsnMetLeuThrTrpArgAlaGluGlnGlyMetGlnPheTrpVal 1125
Db	906	ACCAGATGATTTTAGTAAAGGCTGAAGGAATAGAAAAATCATATTACAAATCCATCTTA 965		
Qy	866	LeuAspLeuThrAspAsnArgLeuGlnSerThrLeuLysThrLeuSerPheSerPhePro	885	1106 GluAlaLeuAsnMetLeuThrTrpArgAlaGluGlnGlyMetGlnPheTrpVal 1125

QY 1229 SerAlaAsnGlyPheGlyPheAlaIleCysGlnLeuAsnValValTyrAsnValLysAla 1248
Db TCCGCAAAATGGTTTGGATTGCTATTGTGCACCTCAATGTTGTAATAATGTGAAGCT 2165
QY 1249 SerGlySerSerArgArgArgSerIleGlnAsnGlnGluAlaPheAspLeuAspVal 1268
Db TC7GGGTCTTCTAGAGACGAAGATCTATCCAAATCAAGAACCTTTGATTAGATGTT 2225
QY 1269 AlaValLysGluAsnLysAspAspLeuAsnHisValAspLeuAsnValCysThrSerPhe 1288
Db GCTGTAAAGAAATAAAGATGATCAATCATGTGGAATTGATGTGTACAGCTTT 2285
QY 1289 SerGlyProGlyArgSerGlyMetAlaLeuMetGluValAsnLeuLeuSerGlyPheMet 1308
Db TCGGGCCCGGTAGAGTGGCTGCTTATGGAAGTTAACTATTAAGTGGCTTTATG 2345
QY 1309 ValProSerGluAlaIleSerLeuSerGluThrValLysLysValGluTyrAspHisGly 1328
Db GTGCCCTCAGAACCAATTTCTCGACGAGACAGTGAAGAAAGTGAATATGATCATGGA 2405
QY 1329 LysLeuAsnLeuTyrLeuAspSerValAsnGluThrGlnPheCysValAsnIleProAla 1348
Db AAACCTCAACCTCTATTAGATTCTGTAATGAAATGAAACCCAGTTTGTGTTAATCTCTGCT 2465
QY 1349 ValArgAsnPhelLysValSerAsnThrGlnAspAlaSerValSerIleValAspTyrTyr 1368
Db GTGAGAAACCTTTAAAGTTTCAATATCCCAAGATGCTTCAGTGTCCATGATGATTACTAT 2525
QY 1369 GluProArgArgGlnAlaValArgSerTyrAsnSerGluValLysLeuSerSerCysAsp 1388
Db GAGCCAAAGAGACAGCGGTGAGAAAGTTACAACTCTGAAAGTGAAGCTGCTCTCTGTGAC 2585
QY 1389 LeuCysSerAspValGlnGlyCysArgProCysGluAspGlyAlaSerGlySerHisHis 1408
Db CTTTGCAGTCAATCCAGGCTGCCGCTCTCTGTGAGGATGAGCTTCAGGCTCCCATCAT 2645
QY 1409 HisSerSerValIlePheIlePheCysPheLysLeuLeuTyrPheMetGluLeuTrpLeu 1428
Db CACTCTTCAGTCAATTTTCTGTTTCAAGCTTCTGTACTTTATGAACTTTGGCTG 2705

RESULT 2

US-10-108-260A-953
; Sequence 953, Application US/10108260A
; Publication No. US20040005560A1
; GENERAL INFORMATION:
; APPLICANT: HELIX RESEARCH INSTITUTE
; TITLE OF INVENTION: No. US20040005560A1el full length cDNA
; FILE REFERENCE: H1-A0106
; CURRENT APPLICATION NUMBER: US/10/108,260A
; NUMBER OF SEQ ID NOS: 5458
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 953
; LENGTH: 2273
; TYPE: DNA
; ORGANISM: Homo sapiens
US-10-108-260A-953

Alignment Scores:

Pred. No.: 0 Length: 2273
Score: 3360.00 Matches: 657
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 45.73% Indels: 0
DB: 16 Gaps: 0

US-10-020-095-4 (1-1428) x US-10-108-260A-953 (1-2273)

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Db 66 ATGACGGGCCCAACCGCTCTGACCGCGCCGCCACCTCTCTGCTGTGACCGCGGCTG 125

QY 21 AlaValAlaProGlyProArgPheLeuValThrAlaProGlyIleIleArgProGlyGly 40
Db GCCGTGGCTCCCGGCGCTCGGTTCCTGTGTGACAGCCCGAGGATCATCAGGCCCGGAGGA 185
QY 41 AsnValThrIleGlyValGluLeuLeuGluHisCysProSerGlnValThrValLysAla 60
Db AATGTGACTATTGGGGTGGAGCTTCTGAAACACTGCCCTTCCACAGGTGACTGTGAAGCG 245
QY 61 GluLeuLeuLysThrAlaSerAsnLeuThrValSerValLeuGluAlaGluGlyValPhe 80
Db GAGCTGCTCAGACAGCATCAAACTCACTGCTCTGCTCTCTGGAAGCAGAGAGAGTCTTT 305
QY 81 GluLysGlySerPheLysThrLeuThrLeuProSerLeuProLeuAsnSerAlaAspGlu 100
Db GAAAAAGGCTCTTTTAAGACACTTACTCTCCATCACTACCTCTCAACAGTSCAGATGAG 365
QY 101 IleTyrGluLeuArgValThrGlyArgThrGlnAspGluIleLeuPheSerAsnSerThr 120
Db ATTATGAGCTACGTGTNACCGAGCTACCCAGAGTATGAGATTTATTCTCTTAATAGTACC 425
QY 121 ArgLeuSerPheGluThrLysArgIleSerValPheIleGlnThrAspLysAlaLeuTyr 140
Db CGCTTATCATTTGAGACCAAGAGAATATCTGCTTCAATCAACAGACAAGCGCTTATAC 485
QY 141 LysProLysGlnGluValLysPheArgIleValThrLeuPheSerAspPheLysProTyr 160
Db AAGCCAAAGCAAGAGTGAAGTTTCGCATTTGTACACTCTTCTCAGATTTTAAAGCCTTAC 545
QY 161 LysThrSerLeuAsnIleLeuIleLysAspProLysSerAsnLeuIleGlnGluTrpLeu 180
Db AAAACCTCTTTAAACATTCATTAAGGACCCCAATCAATTTGATCCAAACAGTGGTTG 605
QY 181 SerGlnGlnSerAspLeuGlyValIleSerLysThrPheGlnLeuSerSerHisProIle 200
Db TCACAAACAAGTATCTTGGAGTCAATTTCCAAAACTTTTACAGCTATCTTCCCATCCAATA 665
QY 201 LeuGlyAspTrpSerIleGlnValGlnValAsnAspGlnThrTyrGlnSerPheGln 220
Db CTTGGTGCCTGCTCTATTCAAGTTCAAGTGAATGACAGACATCACTATCAATCAATTCAG 725
QY 221 ValSerGluTyrValLeuProLysPheGluValThrLeuGlnThrProLeuTyrCysSer 240
Db GTTTTCAGAAATATGATTATACCAAAATTTGAAGTGACTTTGCAGACACCATATATTGTTCT 785
QY 241 MetAsnSerLysHisLeuAsnGlyThrIleThrAlaLysTyrThrTyrGlyLysProVal 260
Db ATGAATCTTAAGCATTTAAATGGTACCATCACGCAAAAGTATACATATGGGAAGCCAGTG 845
QY 261 LysGlyAspValThrLeuThrPheLeuProLeuSerPheTrpGlyLysLysLysAsnIle 280
Db AAAGGAGACGTAAACGCTTACATTTTACCCTTATCTTTTGGGCAAGAGAGAAAAATATT 905
QY 281 ThrLysThrPheLysIleAsnGlySerAlaAsnPheSerPheAsnAspGluGluMetLys 300
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QY 321 ValGluIleLeuThrThrValThrGluSerValThrGlyIleSerArgAsnValSerThr 340
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QY 341 AsnValPhePheLysGlnHisAspTyrIleIleGluPhePheAspTyrThrThrValLeu 360
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QY 361 LysProSerLeuAsnPheThrAlaThrValLysValThrArgAlaAspGlyAsnGlnLeu 380
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QY 381 ThrLeuGluGluArgAsnAsnValIleThrValThrGlnArgAsnTyrThrGlu 400

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; TITLE OF INVENTION: Secreted Polypeptides
; FILE REFERENCE: 805A
; CURRENT APPLICATION NUMBER: US/10/112,944
; CURRENT FILING DATE: 2002-03-28
; PRIOR APPLICATION NUMBER: US 09/488,725
; PRIOR FILING DATE: 2000-01-21
; PRIOR APPLICATION NUMBER: US 09/491,404
; PRIOR FILING DATE: 2000-01-25
; PRIOR APPLICATION NUMBER: US 09/496,914
; PRIOR FILING DATE: 2000-02-03
; PRIOR APPLICATION NUMBER: US 09/515,126
; PRIOR FILING DATE: 2000-02-28
; PRIOR APPLICATION NUMBER: US 09/519,705
; PRIOR FILING DATE: 2000-03-07
; PRIOR APPLICATION NUMBER: US 09/540,217
; PRIOR FILING DATE: 2000-03-31
; PRIOR APPLICATION NUMBER: US 09/552,929
; PRIOR FILING DATE: 2000-04-18
; PRIOR APPLICATION NUMBER: US 09/577,408
; PRIOR FILING DATE: 2000-05-18
; NUMBER OF SEQ ID NOS: 924
; SOFTWARE: pt_FL_genes Version 5.0
; SEQ ID NO 160
; LENGTH: 1880
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: CDS
; LOCATION: (80)..(1867)
; US-10-112-944-160

1206 ACTCTTGAAGAAAGAAATAATAGTATAGTCATACAGTGACACAGAGAAACCTATCTGAG 1265
401 TTTTTPSerGlySerAsnSerGlyAsnGlnLysMetGluAlaValGlnLysIleAsnTyr 420
1266 TACTGGAGCGGATCTAACAGTGGAAATCAGAAATGGAAGCTGTTTCAGAAATAAATAT 1325
421 ThrValProGlnSerGlyThrPheLysIleGluPheProIleLeuGluAspSerGlu 440
1326 ACTGTCCCCAAGTGGAACTTTTAAGATTGAATCCCAATCTCGAGGATCCAGTAG 1385
441 LeuGlnLeuLysAlaTyrPheLeuGlySerLysSerMetAlaValHisSerLeuPhe 460
1386 CTACAGTTGAAGGCTATTTCCTTGGTAGTAAAGTAGCATGGCAGTTTCATGCTGTTT 1445
461 LysSerProSerLysThrTyrIleGlnLeuLysThrArgAspGluAsnIleLysValGly 480
1446 AAGTCTCTAGTAGACATACATCCAACTAAACCAAGAGATGAAATAATAAGGTGGGA 1505
481 SerProPheGluLeuValSerGlyAsnLysArgLeuLysGluLeuSerTyrMetVal 500
1506 TCGCTTTTGGAGTTGGTGTAGTGGCAACAAACGATTGAAGGATTAGCTATATGGTA 1565
501 ValSerArgGlyGlnLeuValAlaValAlaGlyLysGlnAsnSerThrMetPheSerLeuThr 520
1566 GTATCCAGGGGACAGTTGGTGGCTGTAGGAAACAAATTCACAAATGTTCTCTTTAACA 1625
521 ProGluAsnSerTrpThrProLysAlaCysValIleValTyrIleGluAspGly 540
1626 CCAGAAATTTCTTGGACTCCAAAGGCTGTGTAATGTGTATTATATTGAAGATGAGG 1685
541 GluIleSerAspValLeuLysIleProValGlnLeuValPheLysAsnLysIleLys 560
1686 GAAATTTAAGTAGTGTCTTAAATTCCTGTTACGTTGTTTAAATAAGATAAG 1745
561 LeuTyrTrpSerLysValLysAlaGluProSerGluLysValSerLeuArgIleSerVal 580
1746 CTATATTGGAGTAAAGTGAAGCTGACCATCTCGAGAAAGTCTCTCTTAGGATCTCTGTG 1805
581 ThrGlnProAspSerIleValGlyIleValAlaValAspLysSerValAsnLeuMetAsn 600
1806 ACACAGCTTGATCTCATAGTTGGATTGAGCTGTGACAAAGTGTGATCTGATGAT 1865
601 AlaSerAsnAspIleThrMetGluAsnValValHisGluLeuGluLeuTyrAsnThrGly 620
1866 GCCTCTAATGATATTACATGGAATGTCGTCATGAGTTGGAACCTTTATAACACAGGA 1925
621 TyrTyrLeuGlyMetPheMetAsnSerPheAlaValPheGlnGluCysGlyLeuTrpVal 640
1926 TATTATTAGCGAGTTTCATGAATCTTTTTCAGTCTTTCAGGAAATGAGCTCTGGTA 1985
641 LeuThrAspAlaAsnLeuThrLysAspTyrIleAspGlyValTyrAspAsn 657
1986 TTGACACATGCAACCTTCACGAAGGATTAATTGATGGTGTGTTTATGACAAAT 2036

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RESULT 3

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US-10-112-944-160
; Sequence 160, Application 'US/10112944
; Publication No. US20040048249A1
; GENERAL INFORMATION:
; APPLICANT: Tang, Y. Tom
; APPLICANT: Yang, Yonghong
; APPLICANT: Wang, Gezhi
; APPLICANT: Zhang, Jie
; APPLICANT: Ren, Feiyang
; APPLICANT: Xue, Aidong J.
; APPLICANT: Wang, Jian-Rui
; APPLICANT: Wehrman, Tom
; APPLICANT: Ghosh, Malabika
; APPLICANT: Wang, Dunrul
; APPLICANT: Zhao, Qing A.
; APPLICANT: Wang, Zhiwei
; TITLE OF INVENTION: No. US20040048249A1el Nucleic Acids and

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; TITLE OF INVENTION: Secreted Polypeptides
; FILE REFERENCE: 805A
; CURRENT APPLICATION NUMBER: US/10/112,944
; CURRENT FILING DATE: 2002-03-28
; PRIOR APPLICATION NUMBER: US 09/488,725
; PRIOR FILING DATE: 2000-01-21
; PRIOR APPLICATION NUMBER: US 09/491,404
; PRIOR FILING DATE: 2000-01-25
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; PRIOR FILING DATE: 2000-03-07
; PRIOR APPLICATION NUMBER: US 09/540,217
; PRIOR FILING DATE: 2000-03-31
; PRIOR APPLICATION NUMBER: US 09/552,929
; PRIOR FILING DATE: 2000-04-18
; PRIOR APPLICATION NUMBER: US 09/577,408
; PRIOR FILING DATE: 2000-05-18
; NUMBER OF SEQ ID NOS: 924
; SOFTWARE: pt_FL_genes Version 5.0
; SEQ ID NO 160
; LENGTH: 1880
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: CDS
; LOCATION: (80)..(1867)
; US-10-112-944-160

Alignment Scores:
Pred. No.: 3,43e-288 Length: 1880
Score: 2962.50 Matches: 587
Percent Similarity: 96.23% Conservative: 0
Best Local Similarity: 96.23% Mismatches: 2
Query Match: 40.32% Indels: 21
DB: 13 Gaps: 1

US-10-020-095-4 (1-1428) x US-10-112-944-160 (1-1880)

QY 1 MetGlnGlyProProLeuLeuThrAlaAlaHisLeuLeuCysValCysThrAlaAlaLeu 20
DB 80 ATGCAGGCCCCACCGCTCTCTGACCGCCGCCACCTCTCTGGGTGTCACCGCGCGCTG 139
QY 21 AlaValAlaProGlyProArgPheLeuValThrAlaProGlyIleIleArgProGlyGly 40
DB 140 GCCGTGGCTCCCGGCGCTCGGTTCCTGTGACACGCCCGGCGATCATCAGGCCCGGAGGA 199
QY 41 AsnValThrIleGlyValGluLeuLeuGluHisCysProSerGlnValThrValLysAla 60
DB 200 AATGTGACTATTGGGTGGAGCTTCTGGAACTCTCCCTTCACAGGTGACTGTGAAGCG 259
QY 61 GluLeuLeuLysThrAlaSerAsnLeuThrValSerValLeuGluAlaGluGlyValPhe 80
DB 260 GAGCTGCTCAAGACAGCATCAAACTCACTCTCTCTCTGGAAGCAGAGGAGTCTTT 319
QY 81 GluLysGlySerPheLysThrLeuThrLeuProSerLeuProLeuAsnSerAlaAspGlu 100
DB 320 GAAAAAAGCTCTTTTAAGACACTTACTCTTCCATCACTACCTCTGAACAGTGCAGATGAG 379
QY 101 IleTyrGluLeuArgValThrGlyArgThrGlnAspGluIleLeuPheSerAsnSerThr 120
DB 380 ATTTATGAGCTACGTGTAAACCGGACGTACCCAGGATGAGATTTTATCTCTAATAGTACC 439
QY 121 ArgLeuSerPheGluThrLysArgIleSerValPheIleGlnThrAspLysAlaLeuTyr 140
DB 440 CGCTTATCATTTGAGACCAAGAGATATCTGCTTCATTCAACACAGACAGGCGCTTATAC 499
QY 141 LysProLysGlnGluValLysPheArgIleValThrLeuPheSerAspPheLysProTyr 160
DB 500 AAGCAAAAGCAGAGAGTGAAGTTTCGCACTTGTTCAGATTTTTCAGATTTTAAAGCCCTAC 559

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302 CAAAGAAATAGCTTGGTGGTGGTTTGGATCTACTCAGGATACCACTCTGGCTTTAAAGGCT 361
1191 LeuSerGluPheAlaAlaLeuMetAsnThrGluArgThrAsnIleGlnValThrValThr 1210
362 CTGTCTGAAATTCAGCCCTTAATGAATACAGAAAGGACAAATATCCAAGTGACCGTGACG 421
1211 GlyProSerSerProSerPro----- 1217
422 GGGCTAGCTACCAAGTCTCTGTAAGATTTCTGATTGACACACACACACCGCTTACTCCTT 481
1218 -----LeuAlaValGlnProMetAlaValAsnIleSerAlaAsnGlyPhe 1233
482 CAGACAGCAGAGCTGTGTGGTACAGCCAAATGCGAGTTAATATTTCCGCAATGGTTT 541
1234 GlyPheAlaIleCysGlnLeuAsnValValThrAsnValLysAlaSerGlySerSerArg 1253
542 GGATTTGCTATTGTGAGCTCAATGTTGTATATATATGTGNAAGCTTCTGGTCTTCTAGA 601
1254 ArgArgSerIleGlnAsnGlnGluAlaPheAspLeuAspValAlaValLysGluAsn 1273
602 AGACGAAGATCTATCCAAATCAAGAGCCTTTGATTTAGATCTGCTGTAAAGAAAAAT 661
1274 LysAspAspLeuAsnHisValAspLeuAsnValCysThrSerPheSerGlyProGlyArg 1293
662 AAAGATGATCTCAATCAATGATGGAATTTGAATGTGTACAGGCTTTTCGGGCCCGGTAGG 721
1294 SerGlyMetAlaLeuMetGluValAsnLeuLeuSerGlyPheMetValProSerGluAla 1313
722 AGTGGCATGGCTCTTATGGAAGTTAACTATTAAAGTGGCTTTATGGTGGCTTCAGAAGCA 781
1314 IleSerLeuSerGluThrValLysLysValGluThrAspHisGlyLysLeuAsnLeuThr 1333
782 ATTCTCTGAGCGACAGACAGTGAAGAAAGTGGAAATATGATCATGGAAGAACTCAACCTCTAT 841
1334 LeuAspSerValAsnGluThrGlnPheCysValAsnIleProAlaValArgAsnPheLys 1353
842 TTGATTTCTGTAAATGAACCCAGTTTGTGTTAATATCTCTGCTGTGAGAACTTTAAA 901
1354 ValSerAsnThrGlnAspAlaSerValSerIleValAspTyrTyrGluProArgArgGln 1373
902 GTTTCAAATACCCAAAGATGCTTCAGTGTCCATAGTGGATTACTATGAGCAAGACAG 961
1374 AlaValArgSerTyrAsnSerGluValLysLeuSerSerCysAspLeuCysSerAspVal 1393
962 CGCGTGAGAAAGTTACAACTCTGAAGTGAAGCTGTCTCTGAGACCTTTGCGAGTGATGC 1021
1394 GlnGlyCysArgProCysGluAspGlyAlaSerGlySerHisHisSerSerValIle 1413
1022 CAGGCTGCCGTCCTTGTGAGGATGGAGCTTCAGGCTCCCATCATCATCTTTCAGTCAAT 1081
1414 PheIlePheCysPheLysLeuLeuTyrPheMetGluLeuTrpLeu 1428
1082 TTTATTTCTGTTTCAAGCTTCTGTACTTTATGGAACCTTTGGCTG 1126

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RESULT 5

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US-10-276-774-601/c
; Sequence 601, Application US/10276774
; Publication No. US20040053245A1
; GENERAL INFORMATION:
; APPLICANT: Hyseq, Inc.
; APPLICANT: Tang, Y, Tom et al
; TITLE OF INVENTION: No. US20040053245A1el Nucleic Acids and Polypeptides
; FILE REFERENCE: 21272-030
; CURRENT APPLICATION NUMBER: US/10/276,774
; CURRENT FILING DATE: 2002-11-18
; PRIOR APPLICATION NUMBER: 09/560,875
; PRIOR FILING DATE: 2000-04-27
; PRIOR APPLICATION NUMBER: 09/496,914
; PRIOR FILING DATE: 2000-02-03
; NUMBER OF SEQ ID NOS: 2700
; SOFTWARE: Custom
; SEQ ID NO 601
; LENGTH: 1459

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; TYPE: DNA
; ORGANISM: Homo sapiens
US-10-276-774-601
Alignment Scores:
Pred. No.: 9,72e-168 Length: 1459
Score: 1767.50 Matches: 359
Percent Similarity: 94.01% Conservative: 2
Best Local Similarity: 93.49% Mismatches: 1
Query Match: 24.05% Indels: 22
DB: 13 Gaps: 1
US-10-020-095-4 (1-1428) x US-10-276-774-601 (1-1459)
QY 1067 AspValGlnGluSerIleHisPheLeuGluSerGluPheSerArgGlyIleSerAspAsn 1086
DB 1455 GAGGTGCAAGAGTCTATCCATTTTTTGGAGTCTGAATTCAGTAGAGGAATTCAGACAAT 1396
QY 1087 TyrThrLeuAlaLeuIleThrTyrAlaLeuSerSerValGlySerProLysAlaLysGlu 1106
DB 1395 TATACTCTAGCCCTTATAACTTATGCATTATGCATTCAGTGGGAGTCTCTAAAGCGAAGAA 1336
QY 1107 AlaLeuAsnMetLeuThrTrpArgAlaGluGlnGlyGlyMetGlnPheTrpValSer 1126
DB 1335 GCTTTGAATATGCTGACTTGGAGAGCAGACAGAGGTGGCATGCAATTCGGGTGTCA 1276
QY 1127 SerGluSerLysLeuSerAspSerTrpGlnProArgSerLeuAspIleGluValAlaAla 1146
DB 1275 TCAGAGTCCAAACTTCTGACTCTCTGAGCAGCACCGCTCCCTGGGATATTGAAGTTGCAGCC 1216
QY 1147 TyrAlaLeuLeuSerHisPheLeuGlnPheGlnThrSerGluGlyIleProIleMetArg 1166
DB 1215 TATGCACCTGCTCTCACACTTCTTACAAATTCAGACTTCTGAGGGAATCCCAATTTATCAGG 1156
QY 1167 TrpLeuSerArgGlnArgAsnSerLeuGlyGlyPheAlaSerThrGlnAspThrVal 1186
DB 1155 TGGCTAAGCAGGCAAGAAATAGCTTGGTGGTGTTCATCTACTCAGGATACCACCTGTG 1096
QY 1187 AlaLeuLysAlaLeuSerGluPheAlaLeuMetAsnThrGluArgThrAsnIleGln 1206
DB 1095 GCTTTAAAGGCTCTGTCTGAAATTTGAGCCCTTAATGAATACAGAAAGACAAATATCCAA 1036
QY 1207 ValThrValThrGlyProSerSerProSerPro----- 1217
DB 1035 GTGACCGTGACGGGCGCTAGCTCACCAGTCTCTGTAAGTTCCTGATTGACACACACAAC 976
QY 1218 -----LeuAla-ValValGlnProMetAlaVal-AsnIleS 1229
DB 975 CGCTTACTCTTCAGACAGCAGCTTGTGTATGGTACAGCAATGGCAGTGAATATTT 916
QY 1229 erAlaAsnGlyPheGlyPheAlaIleCysGlnLeuAsnValValTyrAsnValLysAla 1249
DB 915 CCGCAAAATGGTTTGGATTTGCTATTTGTCAGCTCAATGTTGTATATAATGTAAGGCTT 856
QY 1249 erGlySerSerArgArgArgSerIleGlnAsnGlnGluAlaPheAspLeuAspVal 1259
DB 855 CTGGGCTCTCTAGAGAGACGAAGATCTATCCAAAATCAAGAGCGCTTTGATTAGATGTTG 796
QY 1269 laValLysGluAsnLysAspAspLeuAsnHisValAspLeuAsnValCysThrSerPheS 1289
DB 795 CTGTAAAAGAAATTAAGATGATCTCAATCATGTGGATTGGAATGTTGTTACAGCTTTT 736
QY 1289 erGlyProGlyArgSerGlyMetAlaLeuMetGluValAsnLeuLeuSerGlyPheMetV 1309
DB 735 CGGGCCCGGGTAGGAGTGGCATGGCTCTTATGGAAGTTAACCTATTAAAGTGGCTTTATGG 676
QY 1309 alProSerGluAlaIleSerLeuSerGluThrValLysLysValGluTyrAspHisGlyL 1329
DB 675 TGCCCTTCAGAGGCAATTTCTCTGAGCGGAGACAGTGAAGAAAGTGAATATGATCATCGAA 616
QY 1329 ysLeuAsnLeuTyrLeuAspSerValAsnGlnThrGlnPheCysValAsnIleProAlav 1349
DB 615 AACTCAACCTCTATTAGATTCTGTAATGAACCCAGTTTGTGTTAATATATTCTCTGCTG 556

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QY 1349 alArgAsnPhelYsValSerThrGlnAspAlaSerValSerIleValAspTyrTrpG 1369
 Db 555 TGAGAACTTTAAAGTTTCAATATACCAAGATCTTCAGTGTCCATAGTGGATTACTATG 496
 QY 1369 luProArgGlnAlaValArgSerTyrAsnSerGluValLysLeuSerSerCysAspL 1389
 Db 495 AGCAAGGAGACAGCGGTGAGAAGTTACAACTCTGAAGTGAAGCTGTCTCTGTGACC 436
 QY 1389 euCysSerAspValGln-GlyCysArgProCysGluAspGlyAlaSerGlySerHisHis 1408
 Db 435 TTTGCAGTGTATGTCAGAGCTGCCGTCTTGTGAGGATGGAGCTTCAGGCTCCCATCAT 376
 QY 1409 HisSerSer--ValIlePhePheCysPheLysLeuLeuTyrPheMetGluLeuTrpL 1428
 Db 375 CACTCTTCGATCGATTTTATTTCTGTTCAGCTTCTGTACTTTATGGAACCTTTGGC 316
 QY 1428 eu 1428
 Db 315 TG 314

RESULT 6

US-10-085-198-29
 ; Sequence 29, Application US/10085198
 ; Publication No. US2004000907A1
 ; GENERAL INFORMATION:
 ; APPLICANT: Alcobrook et al.
 ; TITLE OF INVENTION: Proteins and Nucleic Acids Encoding Same
 ; FILE REFERENCE: 21402-279
 ; CURRENT APPLICATION NUMBER: US/10/085,198
 ; PRIOR FILING DATE: 2002-02-25
 ; PRIOR FILING DATE: 2001-03-16
 ; PRIOR FILING DATE: 2001-02-26
 ; PRIOR FILING DATE: 2001-02-26
 ; PRIOR FILING DATE: 2001-03-16
 ; PRIOR FILING DATE: 2001-08-13
 ; PRIOR FILING DATE: 2001-08-13
 ; PRIOR FILING DATE: 2001-08-16
 ; PRIOR FILING DATE: 2001-08-16
 ; PRIOR FILING DATE: 2001-02-27
 ; PRIOR FILING DATE: 2001-03-20
 ; PRIOR FILING DATE: 2001-03-20
 ; PRIOR FILING DATE: 2001-03-20
 ; PRIOR FILING DATE: 2001-04-21
 ; PRIOR FILING DATE: 2001-06-20
 ; PRIOR FILING DATE: 2001-08-29
 ; PRIOR FILING DATE: 2001-02-28
 ; Remaining Prior Application data removed - See File Wrapper or PALM.
 ; NUMBER OF SEQ ID NOS: 653
 ; SOFTWARE: PatentIn Ver. 2.1
 ; SEQ ID NO 29
 ; LENGTH: 6157
 ; TYPE: DNA
 ; ORGANISM: Homo sapiens
 US-10-085-198-29

Alignment Scores:
 Pred. No.: 5,76e-144 Length: 6157
 Score: 1542.50 Matches: 494
 Percent Similarity: 41.65% Conservative: 257
 Best Local Similarity: 27.40% Mismatches: 555
 Query Match: 20.99% Indels: 497
 DB: 16 Gaps: 57

US-10-020-095-4 (1-1428) x US-10-085-198-29 (1-6157)

QY 5 ProLeuLeuThrAlaAlaHisLeuLeuCysValCys-----ThrAlaAlaLeu 20
 Db 360 CCGTTGCTCCCGCTCTCTGCTCTCTGCTGTGCGCGCGGACGGGTGCGCGCGGAC 419

QY 21 AlaValAlaProGlyProArgPheLeuValThrAlaProGlyIleIleArgProGlyGly 40
 Db 420 CCTCAGGCCCGCGGT-----TACTTGATTCAGCTCCCTCTGTTTTCGCGCGCGCGT 473
 QY 41 AsnValThrIleGlyValGluLeuGluHisCysProSerGlnValThrValLysAla 60
 Db 474 GAGGAAGTCATCAGCGTGCACATCTTT---AACTCTCAAGGGAAGTCAAGTCCAGCT 530
 QY 61 GluLeuLeuLysThrAlaSerAsnLeuThrValSerValLeuGluAlaGluGly--Val 79
 Db 531 CAGCTGGTGGCCCGGCTGAG-----CGGTGGTGCAGAGCCAGGAGGCCCATC 578
 QY 80 PheGluLysGlySerPheLeuThrLeuProSerLeuProLeuAsnSerAlaAsp 99
 Db 579 CTGATAAAGGACAAATCAAA---CTCAAGGTGGCCACCGGCTCCCGGGGCAAGCG--- 632
 QY 100 GluIleTyrGluLeuArgValThrGlyArg-----ThrGlnAspGluIlePhe 116
 Db 633 -----CTTCTGAAAGTGTGGGCGCGCGCTGGCAGGCGGAGGAGGGCCCTCTTT 683
 QY 117 SerAsnSerThrArgLeuSerPheGluThrLysArgIleSerValPheIleGlnThrAsp 136
 Db 684 CACAACACAGACCTCGGTGACCGTGCAGCGCGCGGCGCTTCTGTATTTCATCCAGACG 743
 QY 137 LysAlaLeuTyrLysProLysGlnGluValLysPheArgIleValThrLeuPheSerAsp 156
 Db 744 AAGCTGTGTACAGACCCACGACCGAGTGTCTATAAGCATCTTCACCGCTCTCTCCAAT 803
 QY 157 PheLysProTyrLysThrSerLeuAsnIleLeuIleLysAspProLysSerAsnLeuIle 176
 Db 804 CTGAGGCTGTCAACGAGAACTGGAAGCCTACATCTCTGGACCCCGGAGGCTCTCGGATG 863
 QY 177 GlnGlnTrpLeuSer---GlnGlnSerAspLeuGlyValIleSerLysThrPheGlnLeu 195
 Db 864 ATAGAGTGCAGACACTTAAAGCCGTTCTGTCGCGCATCAACACATGAGCTTCCCTTG 923
 QY 196 SerSerHisProIleLeuGlyAspTrpSerIleGlnValGlnValAsnAspGlnThrTyr 215
 Db 924 TCCGACAGCCTGTGTGGAGATGGTTCAATTTTGTGAATGCAAGGCCAGCGGTAC 983
 QY 216 TyrGlnSerPheGlnValSerGluTyrValLeuProLysPheGluValThrLeuGlnThr 235
 Db 984 AACAACTCTTTGAAGTTTCAGAAGTATGTGTGTCCTCAAGTTTGAAGTTCTGATTGAC 1043
 QY 236 ProLeuTyrCysSerMetAsnSerLysHisLeuAsnGlyThrIleThrAlaLysTyrThr 255
 Db 1044 CCGCGGTATATCCAAGACCTGGACGCTGTGAGACAGGCACTGTGCGGCGCAGGTATACC 1103
 QY 256 TyrGlyLysProValLysGlyAspValThr-----LeuThrPheLeuProSerPhe 273
 Db 1104 TTTGGAAACCTGTGGCTGTGCTTAACGATCAACATGACTGTTAATGGTGTAGGTAC 1163
 QY 274 TrpGlyLysLys-----LysAsnIleThrLysThrPheLysIleAsnGlySerAlaAsn 291
 Db 1164 TACAGCCACGAGTGGGAGCGCTGTCTCAGAACCAACCAAGATCTCTCGGCTCCAGGAC 1223
 QY 292 PheSerPheAsnAspGluGluMetLysAsnValMetAspSerSerAsnGlyLeuSerGlu 311
 Db 1224 TTCACATCTCGGTGAGGACATG-----GlyProValGluIleLeuThrThrVal 1247
 QY 312 TyrLeuAspLeuSerSerPro-----GlyProValGluIleLeuThrThrVal 327
 Db 1248 ---ATCCCGAGCGGACGTCCCTTGACACTTCGCGGCGGAGGTCAGCATCTCGGCCCATGTG 1304
 QY 328 ThrGluSerValThrGlyIleSerArgAsnValSerThrAsnValPhePheLysGlnHis 347
 Db 1305 ACC---AGTGTGACGGGAGCCAGCAG-----GAGTGTGAGGAGGAGGAGGAGGAG 1328
 QY 348 AspTyrIleIleGluPhePheAspTyrThrThrVal-----ThrAlaAlaLeu 20
 Db 1329 -----GTCCGCTTCGATGACTCCACCCCGCTGCGAGGACGAGTGTGTCGATCCGG 1379

Qy 360 -----LeuLysProSerLeuAsnPheThrAlaThrValLys 371
Db 1380 TACTCAAGGACACGAGGAAGCAGATTCAAGCCGGGCTGCTACCTACCTGGGGAAGGTGGAG 1439
Qy 372 ValThrArgAlaAspGlyAsnGlnLeuThrLeuGluArgAsnAsnValValLys 391
Db 1440 CTATCTACCCCGATGGCAGCCCA-----GCTCAGGGGTGACGGTC 1481
Qy 392 ThrValThrGlnArgAsnThrGluTyrTrpSerGlySerAsnSerGlyAsnGlnLys 411
Db 1482 CAGATT-----AAG 1490
Qy 412 MetGluAlaValGlnLysIleAsn-----TyrThr-----ValProGlnSerGlyThr 427
Db 1491 GCAGAGCTGACACCAAGGATACATCTACACAGTGAAGTTGTGCCAGGTGGACTA 1550
Qy 428 PheLysIleGluPheProIleLeuGluAspSerSerGlu-----LeuGlnLeuLys 444
Db 1551 GTGGGGTTTGAAATCCCTCCATCCCGCAGCTCAGCCAGCAGCTGTGGCTGGAGACCAAG 1610
Qy 445 AlaTyrPheLeuGlySerLys-----SerSerMetAlaVal 456
Db 1611 GTATGGCATGTAACCGGAAGCCGGTGGGGCTCAGTACTGCCCCAGCTACCTCTCCCTC 1670
Qy 457 HisSerLeuPheLysSerProSerLysThrTyrIleGlnLeuLysThrArgAspGluAsn 476
Db 1671 GGACGTGGTAC---TCCCCCAGCAGTACTCAGCTGCGAGCCAGCCCTCCACCCA 1727
Qy 477 IleLysValGlySerProPheGluLeuValSerGlyAsnLysArgLeuLys---Glu 495
Db 1728 CTGCAGGTGGGAAGAGCCTATTTCTGTGAAGTCCCATGTCCCTCGCACTTTACC 1787
Qy 496 LeuSerTyrMetValValSerArgGlyGlnLeuValAlaValGlyLysGln----- 512
Db 1788 CTGTACTACAGGTGGCTGCACGGGCAATATGTGTCTATCGGCCAGCAGCTGCCAC 1847
Qy 512 ----- 512
Db 1848 ACCACCCAGCAGCAAGCAAGCGGGCGGCCCTGCCCTGGAGAAACCGATTGTTTAAACA 1907
Qy 513 -----Asn 513
Db 1908 CACCTTTCTGAGACAGAGCCCCACAGCCCGAGAGCTGAGTGCAGCTGTGTGAC 1967
Qy 514 SerThrMetPheSerLeuThrProGluAsnSerTrpThrProLysAlaCysValIleVal 533
Db 1968 TCTCTTCATCTGGCCGTGACCCCC-----AGCATGTCCCTTGTGCTCGCTGTGTC 2021
Qy 534 TyrTyrIleGluAspGlyGluIleIleSerAspValLeuLysIleProValGlnLeu 553
Db 2022 TTCTACCTCAGGAGATGAGAGGGGTCCCGACAGCCCTTCAGTTTCAGTCGAGACC 2081
Qy 554 ValPheLysAsnLysIleLysLeuTyrTrpSerLysValLysAlaGluProSerGluLys 573
Db 2082 TTCTTGGAAACACAGTTTCAGTGACGTATTACAAATGAGACCAACCTGGGGAGGTT 2141
Qy 574 ValSerLeuArgIleSerValThrGlnProAspSerIleValGlyIleValAlaValAsp 593
Db 2142 GTGCACCTGGGATCAGGGCTGCAAGG---GGCAGCTGTGTGTCGCTCGCCGAGTTGAT 2198
Qy 594 LysSerValAsnLeuMetAsnAlaSerAsnAspIleThrMetGluAsnValValHisGlu 613
Db 2199 AAGAGTGTCTACCTGTCTCAGGTCTGGGTTCGGCTGACTCTCCCTCCAGGTTTTCAGGAA 2258
Qy 614 LeuGluLeuTyrAsnThrGly----- 620
Db 2259 CTGGAAGATTATGATGTTTCTGATTCTCTTGGGTGTGCCAGGAGGATGCTTTTGG 2318
Qy 621 -----TyrTyrLeuGly 624
Db 2319 TGGGCTGGGTGAGCGGACCAACGACCGCGGGCTCTCTGTCTTCCCGTGGCCCTGGGGC 2378
Qy 625 MetPheMetAsnSerPheAlaValPheGlnGluCysGlyLeuTrpValLeuThrAsp--- 643

Db 2379 ATCCACAGGACTCTGGTTTGCCTTCACCGAAACGGGACTGGTGTGATGACCGACCGA 2438
Qy 644 AlaAsnLeuThrLysAspTyrIleAspGlyValTyrAspAsnAlaGluTyrAlaGluArg 663
Db 2439 GTGAGCTGAACACACCGCAGGACGCTGCTTAC-----ACCGATGAGGCTGCTCCC 2492
Qy 664 PheMetGluGluAsnGluGlyHisIleValAspIleHisAspPheSerLeuGlySerSer 683
Db 2493 GCTTTCCAGCCCCACACAGGAGCCTGTG-----GCGTGGCTCTCTCC 2537
Qy 684 ProHis-----ValArgLysHisPheProGluThrTrpIleTrp 696
Db 2538 AGGCACCCCCCAGAACACAGAGAGAGAAAGGACTTCTTCCCGAACAATGATGTTGG 2597
Qy 697 LeuAspThrAsnMetGlyTyrArgIleTyrGln---GluPheGluValThrValProAsp 715
Db 2598 CATTGTCTCAACATCAGTACCCCATCTGGTGAAGGACACTCAGTGTGAAGTCCCCGAC 2657
Qy 716 SerIleThrSerTrpValAlaThrGlyPheValIleSerGluAspLeuGlyLeu 735
Db 2658 TCCATCACCAGCTGGTGGTGGTGGCCCTGCTCCACCTCTCAGGCTTAGGCATC 2717
Qy 736 ThrThrThrProValGluLeuGlnAlaPheGlnProPhePheIlePheLeuAsnLeuPro 755
Db 2718 ---GCCGAGCCCTCCCTGCTGAAGACCTTCAAGCCCTTCTCGTGGACTTCATGCTCCCC 2774
Qy 756 TyrSerValIleArgGlyGluPheAlaLeuIleThrIlePheAsnTyrLeuLys 775
Db 2775 GCTCTCATCTCCGTGGGAGCAGTCAAGATCCGCTCAGTGTCTACACTACATCGGC 2834
Qy 776 AspAlaThrGluVal-----LysValIleIleGlyLysSerAspLysPheAspIleLeu 793
Db 2835 ACCTGCGTGAAGTGTACATGAAGCTCTCGTTCGCCAAGGCGCATCCAGTTT--- 2885
Qy 794 MetThrSerSerGluIleAsnAlaThrGlyHis-----GlnGlnThr 807
Db 2886 -----GTTGGGATCTCTGGCAACGCCCATGTGACCAAG 2921
Qy 808 LeuLeuValProSerGluAspGlyAlaThrValLeuPheProIleArgProHisLeu 827
Db 2922 ATGTGTGGCCCCCGGAGGCTGAGCCCATCTGGGTCTGTCTCTCTCTCCTTCAGCGACTG 2981
Qy 828 GlyGluIleProIleThrValThrAlaLeuSer----- 838
Db 2982 GGACTCAACAACATCAGCGCCAAAGCCCTTGTCTTACGAGACACAAATGCTGCGCGGAT 3041
Qy 839 -----ProThrAlaSer 842
Db 3042 GGGAGTCCAGCAACACCCCTGAGGAGAAATCACGCCGACAGGAGGTCCTCCATCGGGTG 3101
Qy 843 AspAlaValThrGlnMetIleLeuValLysAlaGluIleGlyLysSerTyrSerGln 862
Db 3102 GATCAGCTCAGCGCAGTGTGATGTTGAGCGGAGGAGTCCCCCGGCGTACACTAC 3161
Qy 863 SerIleLeu----- 865
Db 3162 AGCGCATTTCTGTCTCCAGTGAGAGAGTCCACATCTCCACCCCAACAAGATGATGATTC 3221
Qy 866 -----LeuAspLeuThr----- 869
Db 3222 CAGTATGTGACGCGCCACTGCGCTCACCGCTTGTGATGTGGTGTGTCGAGCTCACAAT 3281
Qy 870 AspAsnArgLeu----- 873
Db 3282 GATGCCGTGTGGCTTGTCTTCTGGGCCCCAGGACACAGGAGCATGATCGAGATCGTC 3341
Qy 873 ----- 873
Db 3342 CTGGGGGGCATCAGAACACCAGGTTCATGGATCTCCACCAGCAAGATGGGAGAGCCCGTG 3401
Qy 874 -----GlnSerThrLeuLysThrLeuSerPhe----- 882

Db 3402 GCAGTGCACACACGGCCAGATCTCTCTCGGATGAATTCAGAACATTTGGATCAGC 3461
QY 882 ----- 882
Db 3462 TGGCGTGGTGGCCCTTATCCAGGTTGGCCATGGTCCAGAGCCATCCAAATGAGTCTGTCT 3521
QY 882 ----- 882
Db 3522 GTGGCCTGGACCTCCCGAGGCCACACAGAGGTCAGATTCATTGGCTTTTCCACCGGCTGG 3581
QY 882 ----- 882
Db 3582 GGCTCCATGGGTGAATTCGAATCTGGAGGAAGATGGAGGTGACGAGAGCTACAGCGAG 3641
QY 883 -----SerPheProProAsnThrValThrGlySerGluArgValGlnIleThr 898
Db 3642 GCCTTCACCTCGGGTCCACACAGCGGCCATCCCTGGGTCTGAGAGCCACCGCCTCC 3701
QY 899 AlaIleGlyAspValLeuGlyProSerIleAsnGlyLeuAlaSerLeuIleArgMetPro 918
Db 3702 ATCATCGGGAGCTCATGGGGCCAACTGAACACCTCAACACACCTCTCGGCTGGCG 3761
QY 919 TyrGlyCysGlyGluGlnAsnMetIleAsnPheAlaProAsnIleTyrIleLeuAspTyr 938
Db 3762 TTTGGCTGTGGAGAGCAGACATGATCCACTTTGCCACCCAAAGCTTTGTCTGAGTAT 3821
QY 939 LeuThrLysLysLysGlnLeuThrAspAsnLeuLysGluLysAlaLeuSerPheMetArg 958
Db 3822 CTTCAAGAAACCCAGCAGCTCAGCCCTGAGGTGGAGAGAGACACACCTACCTAGTA 3881
QY 959 GlnGlyTyrGlnArgGluLeuLeuTyrGlnArgGluAspGlySerPheSerAlaPheGly 978
Db 3882 CAAGGCTACAGCGCCAGCTGACTCAAGCGCCAGATGGCTCTACAGCGCTTTGGG 3941
QY 979 AsnTyrAspProSerGlySerThrTrpLeuSerAlaPheValLeuArgCysPheLeuGlu 998
Db 3942 GAGCGGACCGCATCGGGAGCATGTGGCTCACAGCTTTGTCTGAAGCTCTTGCACAG 4001
QY 999 AlaAspProTyrIleAspIleAspGlnAsnValLeuHisArgThrTyrThrTrpLeuLys 1018
Db 4002 GCTCGAGCTTTATCTCTGGACCCCGGAGCTGGCTGCCGCCAAGAGCTGGATCATC 4061
QY 1019 GlyHisGlnLysSerAsnGlyGluPheTrpAspProGlyArgValIleHisSerGluLeu 1038
Db 4062 CAGCAGCAGCGCCCATGGCTCTCTCGCCGTGGCAGGCTCTGACAAAGACATC 4121
QY 1039 GlnGlyGlyAsnLysSerProValThrLeuThrAlaTyrIleValThrSerLeuLeu--- 1057
Db 4122 CAGGCTGGATCCACGGCATTTGTCGGCTGACAGCTACGTGTGTGTCTCTCTGGAA 4181
QY 1058 ---GlyTyrArgLysTyrGlnProAsnIleAspValGlnGluSerIleHisPheLeuGlu 1076
Db 4182 ACAGGCACAGCCTCAGAGGAGGAGAGAGGCTCCACTGACAAAGCGAGCATTCTCTGGAG 4241
QY 1077 SerGluPheSerArgGlyIleSerAspAsnTyrThrLeuAlaLeuIleThrTyrAlaLeu 1096
Db 4242 TCTGCTGGCCCTCGGCCATG---GACCTTATAGCTGTGCCCTGACTACCTACGCGCTG 4298
QY 1097 SerSerValGlySerProLysAlaLysGluAlaLeuAsnMetLeuThrTrpArgAlaGlu 1116
Db 4299 ACCCTGCTCGCAGCCCGCAGCCCTGAGGCACTCGCAAGCTCGCTAGCCTGGGCCATC 4358
QY 1117 GlnGluGlyGlyMetGlnPheTrpValSerSerGluSerLysLeuSerAspSerTrpGln 1136
Db 4359 ATCGGAGATGGGTCAACCACTGG-----AGCCTGCAAAATCTCTGGGAC 4403
QY 1137 ProArg-----SerLeu 1140
Db 4404 GTGGACAAGGGCACATTCTTGAAGCTTCAGTGACAGGGGTCTCTCAGTCAGTGTCTCGGC 4463
QY 1141 AspIleGluValAlaAlaTyrAlaLeuLeuSerHisPheLeuGlnPheGlnThrSerGlu 1160
Db 4464 GAGGTGGAATGACAGCTTACGGCCCTCTGACCTACACTCTGTCTGGGTGACGTGGCTGCC 4523

RESULT 7

US-10-085-198-27
; Sequence 27, Application US/10085198
; Publication No. US20040009907A1

QY 1161 GlyIleProIleMetArgTrpLeuSerArgGlnArgAsnSerLeuGlyGlyPheAlaSer 1180
Db 4524 GCCCTGCTGTGGTGAAGTGGCTGTCCAGCAGCGAATGACACTTGGGGTCTTCTCTCC 4583
QY 1181 ThrGlnAspThrThrValAlaLeuLysAlaLeuSerGluPheAlaLeu----- 1197
Db 4584 ACTCAGGACACTGGTGGCTCTCGAGGCTTGGCTGAATATGCAATCTTGTCTCTATGCT 4643
QY 1198 -----Met 1198
Db 4644 GGAGCATCAACCTCACTGTCTCCTGGCCTCCACCACTGGACTACCAGAAACCTTC 4703
QY 1199 AsnThrGluArgThrAsnIleGlnValThrValThrGly-----ProSerSerProSer 1216
Db 4704 GAGCTGCACAGCAACACAGAGGTTCTGCAGACAGCAGCGATCCCGCAGCTCCCCACG 4763
QY 1217 ProLeuAlaValValGlnProMetAlaValAsnIleSerAlaAsnGlyPheGlyPheAla 1236
Db 4764 GGGCTGTTTGTG-----AGTGCCAAAGGGGACGGTGTGTGC 4799
QY 1237 IleCysGlnLeuAsnValValTyrAsnValLys-----AlaSerGlySerSerArg 1253
Db 4800 CTGATGCAGATGTATGTACCTCAATGTGCTGACCGGTGGCCAAAGCCAGCTTTCAG 4859
QY 1254 ArgArgArgSerIleGlnAsnGlnGlu----- 1262
Db 4860 CTGCTCGTAAGCCTCCAGGAGCCTGAGGCCCGCAGGAGCGCCCGCCCTGCTGCCCTCC 4919
QY 1263 -----AlaPheAspLeuAspValAlaValLys 1271
Db 4920 GCAGCTGAGGTTCCCGAGGAGACTGGCCCCAGCTGACGATGATGACCCAGCGCCGAT 4979
QY 1272 GluAsnLysAspAspLeuAsnHisValAspLeuAsnValCysThrSerPheSerGlyPro 1291
Db 4980 CAGCATCACCAAGGAATACAAG---GTGATGTGTGAGGTGTGCACAGGTGTGCTGCATGCA 5036
QY 1292 GlyArgSerGlyMetAlaLeuMetGluValAsnLeuLeuSerGlyPheMetValProSer 1311
Db 5037 GGTCTTCCAATATGCTGTCTCTGAGGTGCCCTGTCTGTCTGAGGCTTCCGGGCGACATC 5096
QY 1312 GluAlaIleSerLeuSerGluThr-----ValLysLysValGlu 1324
Db 5097 GAG-----AGCCTGGAGCAGCTGTCTCTGACAAAGCAGCATGGGGATGAAGAGGTATGAA 5150
QY 1325 TyrIlePheHisGlyLysLeuAsnLeuTyrIleuAspSerVal---AsnGluThrGlnPheCys 1343
Db 5151 GTGCTGGACCGCGAGTGTCTTCTACTTTGATGAGATCCCGCCCGGTGCTGCTGACGTGC 5210
QY 1344 ValAsnIleProAlaValArgAsnPheLysValSerAsnThrGlnAspAlaSerValSer 1363
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QY 1364 IleValAspTyrTyrGluProArgGlnAlaValArgSerTyrAsnSerGluVal--- 1382
Db 5271 GTGTACGACTACTACGAACCGCCTTCGAGGCCACTCGCTTCTACAAGCTCAGCAGCGAC 5330
QY 1383 -----LysLeuSerSerCysAspLeuCysSerAspValGln----- 1394
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QY 1395 -----GlyCysArgProCysGluAspGlyAlaSerGlySerHisHisSer 1410
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QY 1411 SerValIle 1413
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Qy 496 LeuSerTyrMetValValSerArgGlyGlnLeuValAlaValGlyLysGln----- 512
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Qy 512----- 512
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Qy 513-----Asn 513
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Qy 514 SerThrMetPheSerLeuThrProGluAsnSerTrpThrProLysAlaCysValIleVal 533
Db 1630 TCTCTTCACTGCGCGTGCACCC---AGCATGGTCCCTTGGTGGCTGGTGC 1683
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Qy 554 ValPheLysAsnLysIleLysLeuTyrTrpSerLysValLysAlaGluProSerGluLys 573
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Qy 574 ValSerLeuArgIleSerValThrGlnProAspSerIleValGlyIleValAlaValAsp 593
Db 1804 GTCGACCTGGGATCAGGCTGCAAG---GGCAGCTGTGTGTGCTGCGCGCAGTTGAT 1860
Qy 594 LysSerValAsnLeuMetAsnAlaSerAsnAspIleThrMetGluAsnValValHisGlu 613
Db 1861 AAGAGTGTCTACCTGTCTCAGTCTGGGTCCGGCTGACTCCTGCCCAGGTTTTCAGGAA 1920
Qy 614 LeuGluLeuTyrAsnThrGly----- 620
Db 1921 CTGGAAGATTATGATGTTCTGATTCCTTTGGCGTGTCCAGGAGGATGTCCTTTTGG 1980
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Db 2041 ATCACAAGGACTCTGGGTTGGCTTTCACCGAAACGGGACTGGTGTGATGACCGACGA 2100
Qy 644 AlaAsnLeuThrLysAspTyrIleAspGlyValTyrAspAsnAlaGluTyrAlaGluArg 663
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Db 2200 AGGCACCCCCCAGACAGAGAGAGAAAGGACTTCTTCCCCGAAACATGATTTGG 2259
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Db 2497 ACCTCGCTGAGGTGTACATGAAGCTCTCGGTCCCAAGGACCTCCAGTTT----- 2547
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Qy 808 LeuLeuValProSerGluAspGlyAlaThrValLeuPheProIleArgProThrHisLeu 827
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Db 2644 GGACTCAACAACATCAGGCCCAAGCCCTTCTTACGGAGACACAAATTGTCGCGGAT 2703
Qy 839 -----ProThrAlaSer 842
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Db 2884 CAGTATGTGACGCGCCACTGCGCTCACCCTTGTGTTGGTGTGCGAGCTCACAAT 2943
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Qy 873----- 873
Db 3004 CTGGGGGGGCATCAGAACACACAGGTCATGATCTCCACCAGAAAGATGGGAGAGCCGTG 3063
Qy 874 -----GlnSerThrLeuLysThrLeuSerPhe----- 882
Db 3064 GCCAGTGCACACAGCGCAAGATCCTCTCTGGGATGAATTGAGAACATTCGATCAGC 3123
Qy 882----- 882
Db 3124 TGGCGTGTGGCTTATCCAGGTTGGCCATGTCAGAGCCATCCAATGAGTCTGTCTATT 3183
Qy 882----- 882
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Qy 882----- 882
Db 3244 GGCTCATGGGTGAATTCCGAATCTGGAGGAAGATGGAGGTGGACGAGGTACAGCGAG 3303
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Db 3304 GCCTTACCTCTGGGGTCCACAGCGCCCATCCTCTGGTCTGAGCAGGACCCGCTCC 3363
Qy 899 AlaIleGlyAspValLeuGlyProSerIleAsnGlyLeuAlaSerLeuIleArgMetPro 918
Db 3364 ATCATCGGGAGCGTCATGGGGCCAACTGAAACCACTCAACACCTCTCTGGGTGCGG 3423
Qy 919 TyrGlyCysGlyGluGlnAsnMetIleAsnPheAlaProAsnIleTyrIleLeuAspTyr 938
Db 3424 TTTGGCTGTGAGAGCAGAAACATGATCCACTTGCACCCACGCTTGTCTTGAAGTAT 3483


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; PRIOR FILING DATE: 2001-02-28
; Remaining Prior Application data removed - See File Wrapper or PALM.
; NUMBER OF SEQ ID NOS: 653
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 25
; LENGTH: 6195
; TYPE: DNA
; ORGANISM: Homo sapiens
US-10-085-198-25

Alignment Scores:
Pred. No.: 1,2e-142 Length: 6195
Score: 1529.50 Matches: 494
Percent Similarity: 40.87% Conservative: 258
Best Local Similarity: 26.85% Mismatches: 559
Query Match: 20.82% Indels: 529
DB: 16 Gaps: 57

US-10-020-095-4 (1-1428) x US-10-085-198-25 (1-6195)

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QY 21 AlaValAlaProGlyProArgPheLeuValThrAlaProGlyIleleArgProGly 40
Db 82 CCTCAGGCGCGCGGT-----TACTTGTATGAGCTCCCTCTGTTTTCGCGCGCGT 135
QY 41 AsnValThrIleGlyValGluLeuLeuGluHisCysProSerGlnValThrVallyAla 60
Db 136 GAGGAGTCACTAGCTGACCACTTT---AACTCTCAAGGAACTCAGTCCAGGCT 192
QY 61 GluLeuLeuLysThrAlaSerAsnLeuThrValSerValLeuGluAlaGluGly---Val 79
Db 193 CAGCTGGTGGCCCGCAGGTGAG-----CCGCTGTGTCAGAGCCAGGAGCCATC 240
QY 80 PheGluLysGlySerPheLys-----86
Db 241 CTGGATAAAGGACAATCAAACTCAAGCATACGTCCTCAGCACCTCCGGTATCTCCCTC 300
QY 87 -----ThrLeuThrLeuProSerLeuProLeuAsnSerAlaAspGluIleTyr 102
Db 301 CTGCCCATCTCTCCCTGCTCTTGGTGGCGGACCTTTCTCTCTCTCAGCCTCTGG 360
QY 103 Glu-----103
Db 361 CCAGTGTTCAGATATTCCAGAAACAGGCGCAGGTGCCCCAGCGCTCCGCGGCCAAGCG 420
QY 104 ---LeuArgValThrGlyArg-----ThrGlnAspGluIleLeuPheSerAsnSer 119
Db 421 CTTCTGAAGTGTGGGCGCCGCGCTGGCAGCGGAGGAGGCGGCCCTCTTTTCAACACAG 480
QY 120 ThrArgLeuSerPheGluThrLysArgIleSerValPheIleGlnThrAspLysAlaLeu 139
Db 481 ACCTCGTGACCGTGAGCGCGCGCGCTCTGTATTATCAGACGACGACAAGCCTGTG 540
QY 140 TyrLysProLysGlnGluValLysPheArgIleValThrLeuPheSerAspPheLysPro 159
Db 541 TACAGACCCGAGCAGCGAGTGTCTAAGCATCTTCACCGCTCTCTCCAAATCTGAGGCT 600
QY 160 TyrLysThrSerLeuAsnIleLeuIleLysAspProLysSerAsnLeuIleGlnInTrp 179
Db 601 GTCAACGAGAAGCTGGAAGCCTATCTCTGACCCCCCGAGGCTCTCGGATGATAGATGG 660
QY 180 LeuSer---GlnGlnSerAspLeuGlyValIleSerLysThrPheGlnLeuSerSerHis 198
Db 661 AGACACTTAAAGCGGTCTGCTCGGCATCATCAACATGAGCTTCCCTTGTCCGACCA 720
QY 199 ProIleLeuGlyAspTrpSerIleGlnValGlnValAsnAspGlnThrTyrGlnSer 218
Db 721 CTTGTGTGGAGAAGTGTCAATTTTGTGAATGCAAGGCCACCGGTACACAGTCT 780
QY 219 PheGlnValSerGluTyrValLeuProLysPheGluValThrLeuGlnThrProLeuTyr 238
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Db 781 TTTGAAGTTTCAAGATATGTTTCCCAAGTTTCTGAGTTTCTGATGACCCCGCGGTAT 840
QY 239 CysSerMetAsnSerLysHisLeuAsnGlyThrIleThrAlaLysTyrThrGlyLys 258
Db 841 ATCCAAGACCTGACGCGCTGTGACAGAGGCACTGTGCGGCGCAGGTATACCTTTPGGAAA 900
QY 259 ProValLysGlyAsp-----ValThrLeuThrPheLeuProLeuSerPheTrpGlyLys 276
Db 901 CTTGTGGCTGGTCTTAATGATCAATGACTTAAATGCTAGGTAGGTACTACAGCCAC 960
QY 277 Lys-----LysAsnIleThrLysThrPheLysIleAsnGlySerAlaAsnPheSerPhe 294
Db 961 GAGGTGGAGCGCCCTGCTCTCAGAACCAACCAAGATCTCTCGGCTCCCGGAGCTTCGACATC 1020
QY 295 AsnAspGluGluMetLysAsnValMetAspSerSerAsnGlyLeuSerGluTyrLeuAsp 314
Db 1021 TCGGTGAGGACATG-----ATCCCA 1041
QY 315 LeuSerSerPro-----GlyProValGluIleLeuThrValThrGluSer 330
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QY 331 ValThrGlyIleSerArgAsnValSerThrAsnValPhePheLysGlnHisAspTyrIle 350
Db 1099 GTGACGCGGAGCCAGCAG-----1116
QY 351 IleGluPhePheAspTyrThrVal-----359
Db 1117 GTCGGTTCGATGACTCCACCCCGTCAGAGCGAGCTGGTGGACATCCGGTACTCCAAAG 1176
QY 360 -----LeuLysProSerLeuAsnPheThrAlaThrValLysValThrArg 374
Db 1177 GACACGAGGAAGCAGATTCAAGCGGCGCTGACCTGCGGGAAGGTGGAGCTATCTCTAC 1236
QY 375 AlaAspGlyAsnGlnLeuThrLeuGluArgAsnAsnValIleIleThrValThr 394
Db 1237 CCCGATGCGACCCCA-----CCTGAGGGGGTGCAGGTCCAGATT---1275
QY 395 GlnArgAsnTyrThrGluTyrTrpSerGlySerAsnSerGlyAsnGlnLysMetGluAla 414
Db 1276 -----AAGGCAGAGCTG 1287
QY 415 ValGlnLysIleAsn---TyrThr-----ValProGlnSerGlyThrPheLysIle 430
Db 1288 ACACAAAGGATAACATCTACACAGTGAAGTTGTGTCGCCAGCTGAGTACGTGGGTTT 1347
QY 431 GluPheProIleLeuGluAspSerSerGlu-----LeuGlnLeuLysAlaTyrPhe 447
Db 1348 GAAATCCCTCCATCCCACTGAGCCAGCACGTCGTGGTGGAGACCAAGTGTATGSCA 1407
QY 448 LeuGlySerLys-----SerSerMetAlaValHisSerLeu 459
Db 1408 CTGAACGGAAGACCGCTGGGGGCTCAGTACCTGCCCAGCTACCTCTCCCTCGGAGCTGG 1467
QY 460 PheLysSerProSerLysThrTyrIleGlnLeuLysThrArgAspGluAsnIleLysVal 479
Db 1468 TAC---TCCCCAGCCAGTGTACTGAGCTGAGCCACCCCTCCACCCACTGCAGTT 1524
QY 480 GlySerProPheGluLeuValValSerGlyAsnLysArgLeuLys---GluLeuSerTyr 498
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QY 499 MetValValSerArgGlyGlnLeuValAlaValGlyLysGln-----512
Db 1585 GAGGTGGTGCACGGGCGCAATATTGTGTATCGGCGCAGAGCTGCCACACACCACCG 1644
QY 512 -----512
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QY 513 -----AsnSerThrMet 516
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Qy	839	-----ProThrAlaSerAspAlaVal 845	
Db	2839	AGCAAACACCCTCAGGAGAATCACGCCGACAGAGGGTCCCCTCGGGTGGATCACGTC 2898	
Qy	846	ThrGlnMetIleLeuValLysAlaGluGlyVileGluLysSerTyrSerGlnSerIleLeu 865	
Db	2899	AGCGCATGTGATGTTGAGGCGGAAGAGTCCCCCGCGGTACACTACAGCGCATTC 2958	
Qy	865	----- 865	
Db	2959	TTCGTGCCAGTCAGAGAGTCCACATCTCCACCCCAACAAGTATGATGATCCAGTATGTG 3018	
Qy	866	-----LeuAspLeuThr-----AspAsnArg 872	
Db	3019	CAGCGGCACACTGGCCCTCACCCGCTTGATGTGGCTGTGCGAGCTCAATGATGCCGT 3078	
Qy	873	Leu----- 873	
Db	3079	GTCGCCTTGCTTCTGGGCCCCAGGACACAGCAGGCATGATCGAGATCGTCTGGGGGG 3138	
Qy	874	-----Gln 874	
Db	3139	CATCAGAACACCAGGTGATGATCTCCACGACCAAGATGGAGAGCCGTGGCCATGTCA 3198	
Qy	875	SerThrLeuLysThrLeuSerPhe----- 882	
Db	3199	CACACGCCAAGATCCTCTCTGGATGAATTCAGAACATTCTGGATCAGCTGGCGTGT 3258	
Qy	882	----- 882	
Db	3259	GGCCTTATCAGGTGGCCATGTCCAGAGCCATCAATGAGTCTCATGTGGCGCTGG 3318	
Qy	882	----- 882	
Db	3319	ACCTCCGAGGCCACGAGAGGTCAGTTTCTATTGGCTTTTCCACCGCTGGGCTCCATG 3378	
Qy	882	----- 882	
Db	3379	GGTGAATTCGAAATCGAGGAAGATGGAGTGGACGAGAGCTACAGCGAGGCTTCACC 3438	
Qy	883	---SerPheProAsnThrValThrglyserGluargValGlnIleThrAlalleGly 901	
Db	3439	CTGGGGTCCACACGGCGCCATCCCTGGGTCTGACGAGCCACCGCTCCATCATCGGG 3498	
Qy	902	AspValLeuGlyProSerIleAsnGlyLeuAlaSerIleLeuArgMetProTyrGlyCyts 921	
Db	3499	GAGCTCATGGGGCAACCCCTGAACCACTTAACAACCTCTGGCGTGGCGTGTGGCTGT 3558	
Qy	922	GlyGluGlnAsnMetIleAsnPheAlaProAsnIleTyrIleLeuAspTyrIleThrLys 941	
Db	3559	GGAGAGCAGAAATGATCCACTTTCACCCAAACGTCTTTGCTTTGAAGTATCTTCAGAAA 3618	
Qy	942	LysIysGlnLeuThrAspAsnLeuLysGluLysAlaLeuSerPheMetArgGlnGlyTyr 961	
Db	3619	ACCCAGCAGCTCAGCCCTGAGTGGAGAGAGACACCCGACTACTTGTATGACAGGCTAC 3678	
Qy	962	GlnArgGluLeuLeuTyrGlnArgGluAspGlySerPheSerAlaPheGlyAsnTyrAsp 981	
Db	3679	CAGCGCAGCTGACCTACAAGGCCAGGATGGCTCTACAGCGCGTTTGGGAGCGGAC 3738	
Qy	982	ProSerGlySerThrTrpLeuSerAlaPheValLeuArgCysPheLeuGluAlaAspPro 1001	
Db	3739	GCATCGGGGAGCATGGCTTCACAGCCTTTGTCTGAAGTCTTCCGACAGGCTCCGACG 3798	
Qy	1002	TyrIleAspileAspGlnAsnValLeuHisArgThrTyrrThrIleuLysGlyHisGln 1021	
Db	3799	TTTATCTTCGTGACCCCGGAGCTGGTCCGCCCAAGAGCTGGATCATCCAGCAGCAG 3858	


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; PRIOR APPLICATION NUMBER: 60/238,373
; PRIOR FILING DATE: 2000-10-06
; PRIOR APPLICATION NUMBER: 60/238,372
; PRIOR FILING DATE: 2000-10-06
; PRIOR APPLICATION NUMBER: 60/238,383
; PRIOR FILING DATE: 2000-10-06
; PRIOR APPLICATION NUMBER: 60/238,382
; PRIOR FILING DATE: 2000-10-06
; PRIOR APPLICATION NUMBER: 60/275,892
; PRIOR FILING DATE: 2001-03-14
; PRIOR APPLICATION NUMBER: 60/296,860
; PRIOR FILING DATE: 2001-06-08
; NUMBER OF SEQ ID NOS: 200
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 199
; LENGTH: 4492
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: CDS
; LOCATION: (1)..(4374)
US-10-096-625-199

Alignment Scores:
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Score: 1444.50 Matches: 431
Percent Similarity: 44.28% Conservative: 273
Best Local Similarity: 27.11% Mismatches: 571
Query Match: 19.66% Indels: 315
DB: 13 Gaps: 46

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Db 88 CGGTAAATTTCCCTC-----TCCGTCAGAGAGTTGTTGGACCTGAGCCCT 135
Qy 54 SerGlnValThrValLysAlaGluLeuLysThrAlaSerAsnLeuThrValSerVal 73
Db 136 GGTACAGTGATGTTAAATTCACGGTTACTCTGGAGACCAAGGACCAAGCCAGAGTTG 195
Qy 74 LeuGluAlaGluGlyValPheGluLysGlySerPheLysThrLeuThrLeuProSerLeu 93
Db 196 CTAGATACTCTGGACTGGAAGAGAGGACCTTACATTGTATCTCTTCTGTACCACT 255
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Db 256 CTCTGGTGGCACAGAAAGAGTGGCCACAACTCGGGTGTCGGA---GTTGGAATAAC 312
Qy 114 IleLeuPheSerAsnSerThrArgLeuSerPheGluThrLysArgIleSerValPheIle 133
Db 313 ATCAGCTTTCAGGAGAAAGAAAGTTCTAATTCAGAGGAGGAGGAAACGGCACCTTTGTA 372
Qy 134 GlnThrAspLysAlaLeuTyrLysProLysGlnLysValLysPheArgIleValThrLeu 153
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Qy 154 PheSerAspPheLysProTyrLysThrSerLeuAsnIleLeu---IleLysAspProLys 172
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Db 493 AGCAACAGGATTCACAGATGGCTGGAAGTGGTACCTGAGCAAGGCAATGTAGACCTGTC 552
Qy 193 PheGlnLeuSerSerHisProIleLeuGlyAspTrpSerIleGlnValGlnValAsnAsp 212
Db 553 TTCCAACCTGGCACCAGAGGCAATGCTGGGCACCTACACT-----GTGGCAGTGGCTGAG 606

213 GlnThrTyrTyrGlnSerPheGlnValSerGluTyr----- 224
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Qy 225 -----ValLeuProLysPheGluValThrLeuGlnThrProLeuTyrCysSerMet 241
Db 667 CTCCTCTTCAGTGCCTGCCGAAGTTTAAAGTGAAGTGGTGAACCCCAAGAGGATTATCAAG 726
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Qy 302 ValMetAspSerSerAsnGlyLeuSerGluTyrLeuAsp-----LeuSerSer 317
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Qy 318 Pro-----GlyProValGluIle 323
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Qy 364 LeuAsnPheThrAlaThrValLysValThrArgAlaAspGlyAsnGlnLeuThrLeuGlu 383
Db 1096 TTCCCTTCAGTGGAGAGATGCTGCTCAAGTTTCCGCAAGGCGGTGCTCCCTTGCAGAG 1155
Qy 384 GluArgArgAsnValValIle-----ThrVal 393
Db 1156 AACCATCTAGTGTCTTCTGTGATTATATGGCACAATATGAAACCTTCAACCAACCCCTGTT 1215
Qy 394 ThrGlnArgAsn-----TyrThrGluTyrTrpSerGlySerAsn 406
Db 1216 ACTGATACAATAGCCCTAGCTCCCTTTACCTTGGAGACATCCGGTGGATGGACAGAC 1275
Qy 407 SerGlyAsnGlnLysMetGluAlaValGlnLysIleAsnTyrThrValProGlnSerGly 426
Db 1276 -----GTTTCTCTGGAGGGA 1290
Qy 427 ThrPheLysIleGlu-----PheProIleLeuGluAspSer 438
Db 1291 AAGTTTCAATGGAGAGACTTAGTATATATATCCGGAACAAGTGCACCGCTTACTACCAAAAT 1350
Qy 439 SerGluLeuGlnLeuLysAlaTyrPheLeuGlySerLysSerSerMetAlaValHisSer 458
Db 1351 GCCTACCTGCACCTGCGACCTTCTACAGCACAAACCGCAGCTTCTCTGGCATCCACCGG 1410
Qy 459 LeuPheLysSerProSerLysThrTyrIleGlnLeuLysThrArgAspGluAsnIleLys 478
Db 1411 CTA-----AACGGCCCTTGGAA 1428
Qy 479 ValGlySerProPheGluLeuValVal-----SerGly 489
Db 1429 TGTGCCAGCCCCAGGAAGTCTGTGTGATTATTACATCGACCGCGCGATGCAAGCCCT 1488
Qy 490 AsnLysArgLeuLysGluLeuSerTyrMetValValSerArgGlyGlnLeuValAlaVal 509
Db 1489 GACCAAGAGATC---AGCTTCTCTACTATTAAATAGGAAGAAAGTGTGGTATGAG 1545
Qy 510 GlyLysGlnAsn-----SerThrMetPheSerLeu 519

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Qy 1154 LeuGlnPheGlnThrSerGluGluYlleProIleMetArgTrpLeuSerArgGlnArgAsn 1173
Db 3643 ACTCAAAGAGATAGCAAGGAGCCATAGCATAGTGGCTTGGTGGCCAAACAACAT 3702
Qy 1174 SerLeuGlyGlyPheAlaSerThrGlnAspThrValAlaLeuLysAlaLeuSerGlu 1193
Db 3703 GCATATGGGGCTCTCTTCTACTCAGCACTAGTGTCTCTCCAACTCTGGCAA 3762
Qy 1194 PheAla-----AlaLeuMetAsnThrGluArgThrAsnIleGlnValThrValThr----- 1210
Db 3763 TATGCCACTACCGCTACATGCCATCTGAGGAGATCAACCTGCTGTAAATCCACTGAG 3822
Qy 1211 -----GlyProSerProSerProLeuAlaValGln----- 1222
Db 3823 AATTCAGCGCACATTCACATACATAGCTAGTTAAGATTTGATTTTCAGCAGGATACC 3882
Qy 1223 -----ProMetAlaValAsnIleSerAlaAsnGlyPheGlyPheAlaIleCys 1238
Db 3883 CTGCCCAATGTCCTGGAATGTACACGCTGGAGGCTCAGGCCAGGCTGTGTCTATGTG 3942
Qy 1239 GlnLeuAsnValValThrValValValLysAlaSerGlySerSerArgArgArgSerIle 1258
Db 3943 CAGACGGTGTGAGATACAATATCTCCCTCCC----- 3975
Qy 1259 GlnAsnGlnGluAlaPheAspLeuAspValAlaValLys-----GluAsnLys 1274
Db 3976 ACAATATGAGACCTTATGCTTAGTGTGGAATAGAAAGCTAGATGTGAGCAGCCG 4035
Qy 1275 AspAspLeuAsnHisValAspLeuAsnValCysThrSerPheSerGlyPro---GlyArg 1293
Db 4036 ACTTCACCTCGATCTTCGACTCTCATTATTCACACCATGTTATGTGGGAGCCGTAGCTCT 4095
Qy 1294 SerGlyMetAlaLeuMetGluValAsnLeuLeuSerGlyPhe-----MetValProSer 1311
Db 4096 TCCAAATAGCTATGTGGAAGTGAAGATGCTATCTGGGTTTCACTCCATGGAGGCCACC 4155
Qy 1312 GluAlaIleSerLeuSerGlu---ThrValLysLysValGluTrpAspHisGlyLysLeu 1330
Db 4156 AATCAGTTACTTCTCCAGCAACCCCTGCTGAAGAAGGTTGAATTTGGAAGTACACACTT 4215
Qy 1331 AsnLeuTrpLeuAspSerValAsnGluThrGlnPheCysValAsnIleProAlaValArg 1350
Db 4216 AACATTACTTGGATGACTCAATTAAGAACCTCAGACTTACACCTTCCACTACGCCAA 4275
Qy 1351 AsnPheLysValSerAsnThrGlnAspAlaSerValSerIleValAspTrpYrGluPro 1370
Db 4276 AGTGTGCTGTCACCACTTGAACCAACCAACCATCAAGTCTATGACTACTACCTACCA 4335
Qy 1371 ArgArgGlnAlaValArgSerTrpAsnSer-----GluVal 1382
Db 4336 GATGAACAGCACAACATTCAGTATCTCTGATCCCTGTAATGAGGATAGGAGCTGGAAATC 4395
Qy 1383 LysLeuSerSerCysAspLeuCysSerAspValGlnGlyCysArgProCysGluAspGly 1402
Db 4396 CAATTAGTCTCTGTGACATTTACTGGAGGTGGAA----- 4431
Qy 1403 AlaSerGlySerHisHisSerSerVal 1412
Db 4432 -----CATTTCTTGTCTC 4443

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RESULT 10

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US-10-608-397-7
; Sequence 7, Application US/10608397
; Publication No. US20040067512A1
; GENERAL INFORMATION:
; APPLICANT: Kenneth David Becker
; APPLICANT: Gonul Velicelebi
; APPLICANT: Xin Wang
; APPLICANT: Rudolph E. Tanzi
; APPLICANT: Lars Bertram
; APPLICANT: Aleister J. Saunders
; TITLE OF INVENTION: SINGLE NUCLEOTIDE POLYMORPHISMS AND MUTATIONS ON ALPHA-2-MACROGLOB

```

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; FILE REFERENCE: 37481-3323B
; CURRENT APPLICATION NUMBER: US/10/608,397
; CURRENT FILING DATE: 2003-06-26
; PRIOR APPLICATION NUMBER: 10/292,081
; PRIOR FILING DATE: 2002-11-08
; PRIOR APPLICATION NUMBER: 60/337,434
; PRIOR FILING DATE: 2001-11-09
; NUMBER OF SEQ ID NOS: 15
; SOFTWARE: PastSeq for Windows Version 4.0
; SEQ ID NO 7
; LENGTH: 4576
; TYPE: DNA
; ORGANISM: Homo sapiens
US-10-608-397-7

```

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Alignment Scores:
Pred. No.: 6,15e-134 Length: 4576
Score: 1441.00 Matches: 453
Percent Similarity: 46.20% Conservative: 264
Best Local Similarity: 29.19% Mismatches: 551
Query Match: 19.61% Indels: 284
DB: 13 Gaps: 60

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US-10-020-095-4 (1-1428) x US-10-608-397-7 (1-4576)

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Qy 12 LeuLeuCysValCysThrAlaAlaLeuAlaValAlaProGlyProArgPheLeuValThr 31
Db 85 CTCITGGTCTCTCTGCCACAGCGCTCCTCGAATAACCGCAGTATATGTTCTG 144
Qy 32 AlaProGlyIleIleArgProGlyGlyAsnValThrIleGlyValGluLeuGluHis 51
Db 145 GTCCCTCTCTCTCTCCACT---GAGACCACTGAGAAGGGCTGTGCTCTTCTGAGTAC 201
Qy 52 CysProSerGlnValThrValLysAlaGluLeuLysThrAlaSerAsnLeuThrVal 71
Db 202 CTGAATGAGACAGTACTGTGAAGTCTTCTTGGAGTCTGTCCAGGGAAACAGGAGCCTC 261
Qy 72 ---SerValLeuGluAlaGluGly---ValPheGluLysGlySerPheLysThrLeuThr 89
Db 262 TTCACTGACCTGGAGGGGAGAGTACCTCACTGTGTGCGCTTC----- 309
Qy 90 LeuProSerLeuProLeuAsnSerAlaAspGlu-----IleTrpGluLeuArgVal 106
Db 310 -----GCTGTCCCAAGTCTTCATCCATGAGAGAGGATATGTTCTCCTACTGTCCAAAGT 363
Qy 107 ThrGlyArgThrGlnAspGluIleLeuPheSerAsnSerThrArgLeuSerPheGluThr 126
Db 364 AAAGGACCAACCAAGAA-----TTTAAAGAAGCGGACCAACAGTGTGTTAAGAAC 414
Qy 127 LysArgIleSerValPheIleGlnThrAspLysAlaLeuTrpLysProLysGlnGluVal 146
Db 415 GAGGACAGTCTGGTCTTGTCCAGACAGACAAATCAATCTACAAACCCAGGCGACAGTG 474
Qy 147 LysPheArgIleValThrLeuPheSerAspPheLysProTrpLysThrSerLeuAsnIle 166
Db 475 AAATTCGTGTGTCTCCATGATGAAACATTTTCAACCCCTGATGATGATGATGATGATGAT 534
Qy 167 Leu---IleLysAspProLysSerAsnLeuIleGlnThrLeuSerGlnGlnSerAsp 185
Db 535 GTATACATTCAGGATCCCAAGGAAATCGCATCCCAATGGCAGAGTTTCCAGTTAGAG 594
Qy 186 LeuGlyValIleSerLysThrPheGlnLeuSerHisProIleLeuGlyAspTrpSer 205
Db 595 GGTGGCTCAGCAATTTCTTTTCCCTCTCATCAGAGCCCTTCCAGGGCTCCTACAAG 654
Qy 206 IleGlnValGlnValAsnAsp-----GlnThrTrpTrpGlnSerPheGlnValSerGlu 223
Db 655 GTGTGTGTGTACAGAAAGAAATCAGGTGGAGGACAGAGCAC---CCTTTTCCCGTGGAGAA 711
Qy 224 TyrValLeuProLysPheGluValThrLeuGlnThrProLeuTrpCysSerMetAsnSer 243
Db 712 TTGTCTTCTCCAAAGTTTGAAGTACAGTACAGTGCAGCAAGATATACCATCTTGGAA 771

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Db 2713 CTTGAACACGGAAGAAAGACACAGTCATCAAGCCTCTGTGTGGTTGAACCTGAAGGACTA 2772
 Qy 857 GluLysSerTyrSerGlnSerIleLeuLeuAspLeuThrAspAsnArgLeuGlnSerThr 876
 Db 2773 GAGAAGGAACAACTCAACTCCCTACTTTGTCATCAGGTGGTGGAGTTTCT----- 2826
 Qy 877 LeuLysThrLeuSerPheSerPheProAsnThrValThrGlySerGluArgValGln 896
 Db 2827 ---GAAGAAATATCCCTGAAACTGCCACCAATATGTGTAGAGAATCTGCCGAGCTTCT 2883
 Qy 897 IleThrAlaIleGlyAspValLeuGlyProSerIleAsnGlyLeuLaserLeuIleArg 916
 Db 2884 GTCTCAGTTTGGGAGACATATTAGGCTCTGCATGCAAAACACACAAAATCTTCTCCAG 2943
 Qy 917 MetProTyrGlyCysGlyGluGlnAsnMetIleAsnPheAlaProAsnIleTyrIleLeu 936
 Db 2944 ATGCCCTATGGCTGTGGAGAGCAGATATGGTCTCTTGTCTTAACATCTATGACTG 3003
 Qy 937 AspTyrLeuThrLysLysLysGlnLeuThrAspAsnLeuLysGluLysAlaLeuSerPhe 956
 Db 3004 GATATCTAAATGAACACACAGCAGCTTACTCCAGAGATCAAGTCCAAGGCCATTTGCTAT 3063
 Qy 957 MetArgGlnGlyTyrGlnArgGluLeuLeuTyrGlnArgGluAspGlySerPheSerAla 976
 Db 3064 CTCAACACTGGTTACCGAGACAGATTGAACACTAACAACACTATGATGGCTCTACAGCAC 3123
 Qy 977 PheGly---AsnTyrAspProSer---GlySerThrTripleuSerAlaPheValLeuArg 994
 Db 3124 TTTGGGAGCGATATGCGAGCAACAGGCGCAACACCTGGCTCACAGCCTTTGTCTTGAAG 3183
 Qy 995 CysPheLeuGluAlaAspProTyrIleAspIleAspGlnAsnValLeuIleArgThrTyr 1014
 Db 3184 ACTTTTCCCAAGCTCGAGCTCATCTTCATCGATGAAGCACACATATCCCAAGCCCTC 3243
 Qy 1015 ThrTripleuLysGlyHisGlnLysSerAsnGlyGluPheTyrAspProGlyArgValIle 1034
 Db 3244 ATATGGCTCTCCAGAGCGAGAGCAATGGCTGTTTCAGGAGCTCTGGGTCACTGCTC 3303
 Qy 1035 HisSerGluLeuGlnGlyAsnLysSerProValThrLeuThrAlaTyrIleValThr 1054
 Db 3304 AACAAATGCCATAAAGGAGGAGTAGAAGATGAAGTGAAGTCTCCGCTTATATCACCATC 3363
 Qy 1055 SerLeuLeuGlyTyrArgLysTyrGlnProAsnIleAspValGlnGluSerIleHisPhe 1074
 Db 3364 GCCCTCTGGAGATCTCTCACAGTCACCTGCTGTGTGCGAATGCCCTGTTTGC 3423
 Qy 1075 LeuGluSer-----GluPheSerArgGlyIleSerAspAsnTyrThr 1088
 Db 3424 CTGGAGTCAGCTGGAAGACAGCACAAAGAGGGACCATGGC---AGCCATGTATATATAC 3480
 Qy 1089 LeuAlaLeuIleThrTyrAlaLeuSerSerValGlySer---ProLysAlaLysGluAla 1107
 Db 3481 AAAGCACTGTGGCTATGCTTTTGGCTCGAGGTAAACGAGACAGAGAGGAAGTA 3540
 Qy 1108 LeuAsnMetLeuThrTyrArgAlaGluGlnGlyGlyMetGlnPheThr----- 1124
 Db 3541 CTCAGTCACTTAATAGGAGAGCTGTGAAGAAAGACAACTCTGCTTGGAGGCCCT 3600
 Qy 1125 ValSerSerGluSerLysLeuSerAspSerTyrGlnProArg-----SerLeuAspIle 1142
 Db 3601 CAGAAACCCAGGACACAGTGGGCGCATTTTTCAGAACCCCGAGCTCCCTGCTGAGGTG 3660
 Qy 1143 GluValAlaAlaTyrAlaLeuSerHisPheLeuGlnPheGln-----ThrSer 1159
 Db 3661 GAGATGATCCTATGTCTCTCGCT---TATCTCAGCGCCCGAGCGCCCAACTCG 3717
 Qy 1160 GluGlyIlePro-----IleMetArgTripleuSerArgGlnArgAsnSerLeu 1175
 Db 3718 GAGGACCTGACCTCTGCAACCAACATCTGTGAAGTGGATCACGAAGCAGCAGATGCGCAG 3777
 Qy 1176 GlyGlyPheAlaSerThrGlnAspThrThrValAlaLeuLysAlaLeuSerGluPheAla 1195
 Db 3778 GCGCGTTTCTCTCCACCCAGGACACAGTGGTGGCTCTCCATGCTCTGTCTCAATATGGA 3837

Qy 1196 AlaLeuMetAsnThrGluArgThrAsnIleGlnValThrValThrGlyProSerSerPro 1215
 Db 3838 GCAGCCACATTTACC---AGGACTGGGAAGGCTGCACAGGTGACTATCCAGTCTTCAGGG 3894
 Qy 1216 SerProLeuAlaValValGln----- 1222
 Db 3895 ACATTTTCCAGCAAAATTCCAAGTGGACAAACACCGCCTGTACTGACAGAGGTCTCA 3954
 Qy 1223 -----ProMetAlaValAsnIleSerAlaAsnGlyPheGlyPheAlaIleCys 1238
 Db 3955 TTGCCAGAGCTGCTGGGAATACAGCATGAAAGTGCACAGAGAGGATGTGTCTACCTC 4014
 Qy 1239 GlnLeuAsnValValTyrAsnValLysAlaSerGlySerSerArgArgArgSerIle 1258
 Db 4015 CAGACATCTTGAATAACAATATT-----CTC 4041
 Qy 1259 GlnAsnGlnGluAlaPheAspLeuAspValAlaValLys-----GluAsnLysAsp 1275
 Db 4042 CCAGAAAGGAGAGTTCCTCTTTAGGAGTGAGACTCTGCCTCAAACTTGTGAT 4101
 Qy 1276 AspLeuAsn---HisValAspLeuAsnValCysThrSerPheSerGlyProGly----- 1292
 Db 4102 GAACCCAAAGCCACACAGCCTTCCAAATCTCCCTAAGTGTCACTTACACAGGAGCGCG 4161
 Qy 1293 ---ArgSerGlyMetAlaLeuMetGluValAsnLeuSerGlyPheMetValProSer 1311
 Db 4162 TCTGCCCTCAACATGGCGATGTTGATGTGAAGATGCTCTGTGGCTTCATTCCTCQAAG 4221
 Qy 1312 GluAlaIleSerLeu-----SerGluThrValLysLysValGluTyrAspHisGly 1328
 Db 4222 CCAACAGTGAAGTCTTGAAGATCTTAACATGTGAGCGGACAGAGTCAGCAGCAAC 4281
 Qy 1329 LysLeuAsnLeuTyrLeuAspSerValAsnGluThrGlnPheCysValAsnIleProAla 1348
 Db 4282 CATGCTTGTATTTACCTTGATAGTGTCAAAATCAGACACTGAGCTTGTTCACCGTT 4341
 Qy 1349 ValArgAsnPheLysValSerAsnThrGlnAspAlaSerValSerIleValAspTyrTyr 1368
 Db 4342 CTGAAGATGTCCAGTAAGAGATCTGAACACCGCATAGTGAAGTCTATGATTACTAC 4401
 Qy 1369 GluProArgArgGlnAlaValArgSerTyrAsnSer 1380
 Db 4402 GAGACGGATGAGTTTGAATTTGCTGAGTACAAATGCT 4437

RESULT 11

US-10-292-081A-7
 ; Sequence 7, Application US/10292081A
 ; Publication No. US20030162202A1

; GENERAL INFORMATION:
 ; APPLICANT: Kenneth David Becker
 ; APPLICANT: Gonul Velicelebi

; APPLICANT: Xin Wang
 ; APPLICANT: Randolph E. Tanzi

; APPLICANT: Lars Bertram
 ; APPLICANT: Aigister J. Saunders

; TITLE OF INVENTION: SINGLE NUCLEOTIDE POLYMORPHISMS AND MUTATIONS ON ALPHA-2-MACROGLO
 ; FILE REFERENCE: 37481-3323

; CURRENT APPLICATION NUMBER: US/10/292,081A
 ; CURRENT FILING DATE: 2002-11-08

; PRIOR APPLICATION NUMBER: 60/337434
 ; PRIOR FILING DATE: 2001-11-09

; NUMBER OF SEQ ID NOS: 15
 ; SOFTWARE: FastSeq for Windows Version 4.0

; SEQ ID NO 7
 ; LENGTH: 4576

; TYPE: DNA
 ; ORGANISM: Homo sapiens

US-10-292-081A-7

Alignment Scores:

6.15e-134 Length: 4576
 1441.00 Matches: 453

Percent Similarity:	46.20%	Conservative:	264	
Best Local Similarity:	29.19%	Mismatches:	551	
Query Match:	19.61%	Indels:	284	
DB:	15	Gaps:	60	
US-10-020-095-4 (1-1428) x US-10-292-081A-7 (1-4576)				
QY	12	LeuLeuCysValCysThrAlaAlaLeuAlaValAlaProGlyProArgPheLeuValThr	31	
DB	85	CTCTTGCTCTCTGCCACAGACGCTCAGTCTCTGGAAACCCGAGTATATGTTCTG	144	
QY	32	AlaProGlyIleIleArgProGlyGlyAsnValThrIleGlyValGluLeuGluHis	51	
DB	145	GTCCCTCTCCTGCTCCACACT---GAGACCCTGAGAAGGCTGTGCTCTCTGAGCTAC	201	
QY	52	CysProSerGlnValThrValLysAlaGluLeuLeuLysThrAlaSerAsnLeuThrVal	71	
DB	202	CTGAATGAGACAGTGAAGTCTCTTGGAGTCTGTGAGGAAACAGAGGCGCTC	261	
QY	72	---SerValIleGluAlaGluGly---ValPheGluLysGlySerPheLysThrLeuThr	89	
DB	262	TTCACTGACCTGGAGCGGAGAAATGACGTATCCACTGTGTGCGCTTC-----	309	
QY	90	LeuProSerLeuProLeuAsnSerAlaAspGlu-----IleTyrGluLeuArgVal	106	
DB	310	-----GCTGTCCCAAGTCTTCATCCAATGAGGAGGTAATGTTCTCTCACTGTCCAAGTG	363	
QY	107	ThrGlyArgThrGlnAspGluIleLeuPheSerAsnSerThrArgLeuSerPheGluThr	126	
DB	364	AAAGGACCAACCCAGAA-----TTTAAGACGGGACACAGTGTGTTAAGAAC	414	
QY	127	LysArgIleSerValPheIleGlnThrAspLysAlaLeuTyrLysProLysGlnGluVal	146	
DB	415	GAGGACAGCTGCTCTTGTCCAGACAGACAATCAATCTACAAACCCAGGSCACAGTG	474	
QY	147	LysPheArgIleValThrLeuPheSerAspPheLysProTyrLysThrSerLeuAsnIle	166	
DB	475	AAATTTGCTGTTCTCCATGGATGAAACTTTCAACCCCTGGAATGAGTTGATTCACCTA	534	
QY	167	Leu---IleLysAspProLysSerAsnLeuIleGlnThrLeuSerGlnGlnSerAsp	185	
DB	535	GTATACATTCAGATCCCAAGAAATCGCATCGCACATGGCAGAGTTTCAGTTAGAG	594	
QY	186	LeuGlyValIleSerLysThrPheGlnLeuSerSerHisProIleLeuGlyAspTrpSer	205	
DB	595	GGTGGCTCAAGCAATTTCTTTTCCCTCTCATCAGAGCCCTTCCAGGCTCTCTACAAG	654	
QY	206	IleGlnValGlnValAsnAsp-----GlnThrTyrTyrGlnSerPheGlnValSerGlu	223	
DB	655	GTGGTGTACAGAAAGAAATCAGGTGGAAGGACAGACAC---CCTTTCCCGTGGAGGAA	711	
QY	224	TyrValLeuProLysPheGluValThrLeuGlnThrProLeuTyrCysSerMetAsnSer	243	
DB	712	TTTGTCTTTCCCAAGTTTGAAGTACAAGTAACAGTGCCCAAGAAATACCATCTTGAA	771	
QY	244	LysHisLeuAsnGlyThrIleThrAlaLysTyrThrTyrGlyLysProValLysGlyAsp	263	
DB	772	GAAGAGATGAATGTATCAGTGTGTGGCCTATACACATATGGGAAGCTGTCCCTGGACAT	831	
QY	264	ValThrLeuThrPheLeuProLeu-----	271	
DB	832	GTGACTGTGAGCATTTGCAGAAAGTATAGTACGCTTCCGACTGCCACCGTGAAGATCA	891	
QY	272	-----SerPheTrpGlyLys	276	
DB	892	CAGGCTTCTGTGAGAAATTCAGTGGACAGCTAAACAGCCATGGCTGTCTCTATCAGCAA	951	
QY	277	LysLysAsnIleThrLysThrPheLysIleAsnGlySerAlaAsnPheSerPheAsnAsp	296	
DB	952	GTAAAA-----ACCAAGGTCTTCCAGCTGAAGAG-----AAGGAG	987	
QY	297	GluGluMetLysAsnValMetAspSerSerAsnGlyLeuSerGluTyrLeuAspLeuSer	316	
DB				
988	TATGAATGAAA-----	CTTACACTGAGGCCAGATCCAA	1023	
317	SerProGlyProValGluIleLeuThr-----	ThrValThrGluSerVal	331	
DB	1024	GAAGAAGGACACAGTGGTGAATTCAGTGAAGGAGGAGTGAATTCACAAGAACCATA	1083	
QY	332	ThrGlyIleSerArgAsnValSerThrAsnValPhePheLysGlnHisAspTyrIleIle	351	
DB	1084	ACCAAACTCTCA---TTTGTGAAAGTGAGACTCACACTTTTCAGACGGA-----ATT	1131	
QY	352	GluPhePheAspTyrThrThrValLeuLysProSerLeuAsnPheThrAlaThrValLys	371	
DB	1132	CCCTTCTTTGGG-----	CAG	1146
QY	372	ValThrArgAlaAspGlyAsnGlnLeuThrLeuGluArgArgAsnAsnValValIle	391	
DB	1147	GTGGCCCTAGTAGTGGAAAGCGCTCCCTATATCA-----AATAAAGTACATA	1194	
QY	392	ThrValThrGlnArgAsnTyrThrGluTyrTrpSerGlySerAsnSerGlyAsnGlnLys	411	
DB	1195	TTCAATC---AGAGGAATGAAGCAACTATATAC-----TCCATGTACACCGATGAG	1245	
QY	412	MetGluAlaValGln---LysIleAsnTyrThr-----ValProGlnSerGlyThrPhe	428	
DB	1246	CATGGCTTTGACAGTTCTCTATCAACACCACTAATGTTATGGGTACTCTCTTACTGTT	1305	
QY	429	LysIleGluPhePro-----IleLeuGluAspSer	438	
DB	1306	AGGTCAATTAACAGGATCGTAGTCCCTGTGTACGGTACCACTGGGTGTGAGAGAACAC	1365	
QY	439	SerGluLeuGlnLeuLysAlaTyrPheLeuGlySerLysSerMetAlaValHisSer	458	
DB	1366	GAAGAGGCACATCAGCTGCTTAT-----	1389	
QY	459	LeuPheLysSerProSerLysThrTyrIleGlnLeuLysThrArgAspGluAsnIleLys	478	
DB	1390	CTTGTGTTCTCCCAAGCAGAGCTTTGTCCACCTTGAGCCCATGTCTCATGAATACCC	1449	
QY	479	ValGlySer-----ProPheGluLeuValValSerGlyAsnLys-----Arg	492	
DB	1450	TGTGGCCATCTCAGACAGTCCAGGCACATTTATTTCTGAATGGAGCACCCTGCTGGGG	1509	
QY	493	LeuLysGluLeuSer-----TyrMetValValSerArgGlyGlnLeuValAlaValGly	510	
DB	1510	CTGAAGAGAGCTCTCCTCTTATTTATCTGATATGCAAGGAGGAGCATTTGTCGAACTGGG	1569	
QY	511	-----LysGlnAsnSerThr-----MetPheSerLeuThr	520	
DB	1570	ACTCATGAGCTGCTGTGAAGCAGAGACATGAGGGCCATTTTCCATCTCATCCCT	1629	
QY	521	ProGluAsnSerTrpThrProLysAlaCysValIleValTyrTyrIleGluAspGly	540	
DB	1630	GTGAAGTCAGACATTCCTCTGCTGCTCGTTCATCTATGCTATGCTTTTACCTACCGGG	1689	
QY	541	GluIleIleSerAspValLeuLysIleProValGlnLeuValPheLysAsnLysIleLys	560	
DB	1690	GACGTGATGGGATTCGCAAAATATGATGTTGAAAATTCGTCGGCCCAACAGGTGGAT	1749	
QY	561	LeuTyrTrpSerLysValLysAlaGluProSerGluLysValSerLeuArgIleSerVal	580	
DB	1750	TTGAGCTTCAGCCCATCACAAGTCTCCAGCCTCACAGGCCACCTGCGAGTCACAGCG	1809	
QY	581	ThrGlnProAspSerIleValGlyIleValAlaValAspLysSerValAsnLeuMet---	599	
DB	1810	GCT---CCTCAGTCGTGCGCCCTCCGTCGTGTGGACCAAGCGTGTGCTCATGAAG	1866	
QY	600	-----AsnAlaSer-----	602	
DB	1867	CCTGATGCTGAGCTCTCGGCGTCTCTCGGTTTACAACCTGTCTACAGAAAAGGACCTCACT	1926	
QY	603	-----AsnAspIleThrMetGluAsnValValHisGluLeuGluLeu	616	
DB	1927	GGCTTCCCTGGCCCTTTTGAATGACAGCAATGAAGACTGCATCAATCGTCAATATGTC	1986	

Qy 617 TyrAsnThrGlyTyr---TyrLeuGlyMetPheMetAsnSer-----PheAla 631
Db 1987 TATATTAAATGAATACATATATCTCCAGTATCAAGTACAAATGAAAAGGATATGTACAGC 2046
Qy 632 ValPheGlnGlyCysGlyLeuThrValLeuThrAspAlaAsnLeuThrLysAspTyrIle 651
Db 2047 TTCTAGAGACATGGGCTTTAAAGGCATTCCACCACTCAAAAGATTGCTAAACCCAAATG 2106
Qy 652 AspGlyValTyrAspAsnAlaGlu-----Tyr 660
Db 2107 TGTCACAGCTTCAACAGTATGAAATGCATGGACCTGAGGCTACGTGTAGGTTTAT 2166
Qy 661 AlaGluArgPheMetGluGluAsnGluGlyHisIleValAspIleHisAspPheSerLeu 680
Db 2167 GAGTCAGATGTAATGGAGAGGCCATGCACGCCGTGTGTCATGTTGAAGAG----- 2217
Qy 681 GlySerSerProHis-----ValAlaGlyHisPheProGluThrTrpIleTrpLeu 697
Db 2218 -----CCTCACGGAGACCGTACGAAAGTACTTCCCTGAGACATGGATCTGGAT 2268
Qy 698 AspThrAsnMetGlyTyrArgIleTyrGlnGluPheGluValThrValProAspSerIle 717
Db 2269 TTGGTGGTGAATAACTCAGCAGGTGTGGCTGAGGTAGGATTAACAGTCCCTGCACACCATC 2328
Qy 718 ThrSerTrpValAlaThrGlyPheValIleSerGluAspLeuGlyLeuGlyLeuThrThr 737
Db 2329 ACCGAGTGAAGCAGCGGGCTTCTCGCTGTCTGAAGATGCTGGACTTGGTATCTCTCC 2388
Qy 738 ThrProValGluLeuGlnAlaPheGlnProPheIlePheLeuAsnLeuProTyrSer 757
Db 2389 ACT---GCCCTCTCCGAGCTTCCAGCCCTTCTTTGTGGAGCTCACATGCCCTACTCT 2445
Qy 758 ValIleArgGlyGluGluPheAlaLeuGluIleThrIlePheAsnTyrLeuLysAspAla 777
Db 2446 GTGATTCTGTGAGAGGCTTTCACACTCAAGCCACCGCTCTTAACACTACCTTCCCAATGC 2505
Qy 778 ThrGluValLysValIleIleGluLysSerAspLysPheAspIleLeuMetThrSerSer 797
Db 2506 ATCCGGTCTAGTGTCAGCTGGAGGCTCTCCCGCTTCTAGCTGTCCAGCTGGAGAG 2565
Qy 798 Glu-----IleAsnAlaThrGlyHisGlnGlnThrLeuLeuValProSer 812
Db 2566 GAACAAGCGCTCACTGCTACTGTGCAACCGGCGGCAA----- 2604
Qy 813 GluAspGlyAlaThrValLeuPheProIleArgProThrHisLeuGlyGluIleProIle 832
Db 2605 -----ACTGTGTCTCGGCGAGTAACCCCAAGTCAATAGGAATGGAATTTC 2652
Qy 833 ThrValThrAlaLeuSer-----ProThrAla 841
Db 2653 ACTGTAGCGCAGAGGCACTAGAGTCTCAAGAGCTGTGTGGAGTCAAGTGCCTTCAGTT 2712
Qy 842 -----SerAspAlaValThrGlnMetIleLeuValLysAlaGluGlyIle 856
Db 2713 CCTGAACACGGAAGGAACACAGTCAATCAAGCCTCTGTGTGTTGAACCTGAAGGACTA 2772
Qy 857 GluLysSerTyrSerGlnSerIleLeuLeuAspLeuThrAspAsnArgLeuGlnSerThr 876
Db 2773 GAGNAGGAACAACATTCACCTCCCTCTTGTCCATCAGGTGGTGGTTCCT----- 2826
Qy 877 LeuLysThrLeuSerPheSerPheProAsnThrValThrGlySerGluArgValGln 896
Db 2827 ---GAAGAATTATCCCTGAAACTGCCACCAATGTGTAGAGAAATCTGCCGAGCTTCT 2883
Qy 897 IleThrAlaIleGlyAspValLeuGlyProSerIleAsnGlyLeuAlaSerLeuIleArg 916
Db 2884 GTCTCAGTTTTGGAGACATATTAGGCTGTCCATGCAAAACACACAAATCTTCTCCAG 2943
Qy 917 MetProTyrGlyCysGlyGluGlnAsnMetIleAsnPheAlaProAsnIleTyrIleLeu 936
Db 2944 ATGCCCTATGGCTGTGGAGAGCAATATGCTCTCTTTGCTCTTAACATCTATGTACTG 3003

Qy 937 AspTyrIleThrLysLysLysGlnLeuThrAspAsnLeuLysGluLysAlaLeuSerPhe 956
Db 3004 CATTATCTAAATGAACACACAGCAGCTTACTCCAGAGATCAAGTCCCAAGGCCATTTGGGTAT 3063
Qy 957 MetArgGlnGlyTyrGlnArgGluLeuLeuTyrGlnArgGluAspGlySerPheSerAla 976
Db 3064 CTCACACTGTTTACAGAGACAGTGAACACTACAACTACTGATGGCTCTCAGACACC 3123
Qy 977 PheGly---AsnTyrAspProSer---GlySerThrTrpLeuSerAlaPheValLeuArg 994
Db 3124 TTGGGAGCGATATGCGAGGAACAGGCAACACCTGGCTCAGAGCTTTGTCTGAAG 3183
Qy 995 CysPheLeuGluAlaAspProTyrIleAspIleAspGlnAsnValLeuHisArgThrTyr 1014
Db 3184 ACTTTTGGCCAAAGTCTGAGCCTTACTCTTCACTGATGAAGCACACATTACCAAGCCCTC 3243
Qy 1015 ThrTrpLeuLysGlyHisGlnLysSerAsnGlyLeuPheTrpAspProGlyArgValIle 1034
Db 3244 ATATGGCTCTCCAGAGCGCAGAGGACAAATGGCTGTTTTCAGAGCTCTGGGTCACTGCTC 3303
Qy 1035 HisSerGlnLeuGlnGlyGlyAsnLysSerProValThrLeuThrAlaTyrIleValThr 1054
Db 3304 AACAAATGCCATAAAGGAGGAGTAGAAGATCAAGTGAACCTCTCCGCTATATACCATC 3363
Qy 1055 SerLeuLeuGlyTyrArgLysTyrGlnProAsnIleAspValGlnGluSerIleHisPhe 1074
Db 3364 GCCCTTCTGGAGATCTCTCTCACAGTCACTCACCTGTTGTCGCAATGCCCTGTTTTCG 3423
Qy 1075 LeuGluSer-----GluPheSerArgGlyIleSerAspAsnTyrThr 1088
Db 3424 CTGGAGTCAGCCTCGAAGACAGACGACAAGAAGGGACCATGCG---AGCCATGATATATACC 3480
Qy 1089 LeuAlaLeuIleThrTyrAlaLeuSerSerValGlySer---ProLysAlaLysGluAla 1107
Db 3481 AAAGCAGTCTGGCCTATGCTTTGCTGGCAGGTAAACAGACAGAGAGAGGAAGTA 3540
Qy 1108 LeuAsnMetLeuThrTrpArgAlaGluGlnGlyGlyMetGlnPheTrp----- 1124
Db 3541 CTCAAGTCACTTAATAGGAAGCTGTGAAGAAAGACAACCTCTGTCCATTTGGAGCGCCT 3600
Qy 1125 ValSerSerGluSerLysLeuSerAspSerTrpGlnProArg-----SerLeuAspIle 1142
Db 3601 CAGAAACCAAGGACACAGTGGGCGCATTTTACGAACCCAGCAGCTCCTCTGTGAGGTG 3660
Qy 1143 GluValAlaAlaTyrAlaLeuLeuSerHisPheLeuGlnPheGln-----ThrSer 1159
Db 3661 GAGATGACATCTATGCTCTCTCGCT---TATCTCAGCGCCAGCCAGCCGCCAACCTCG 3717
Qy 1160 GluGlyIlePro-----IleMetArgTrpLeuSerArgGlnArgAsnSerLeu 1175
Db 3718 GAGGACCTGACCTCTGCAACCAACATCGTGAAGTGGATCAGAGCAGAGAGATGCCAG 3777
Qy 1176 GlyGlyPheAlaSerThrGlnAspThrThrValAlaLeuLysAlaLeuSerGluPheAla 1195
Db 3778 GCGGTTTCTCTCCACCCAGGACACAGTGGTGGCTCTCCATGCTCTCCAAATATGGA 3837
Qy 1196 AlaLeuMetAsnThrGluArgThrAsnIleGlnValThrValThrGlyProSerSerPro 1215
Db 3838 GCAGCCACATTTACC---AGGACTGGGAAGGCTGCACAGGTGACTATCCATGCTTTCAGGG 3894
Qy 1216 SerProLeuAlaValValGln----- 1222
Db 3895 ACATTTTCCAGAAATTCCAAGTGGACAAACAAACCGCCTGTACTGTCAGCAGGTCTCA 3954
Qy 1223 -----PrometAlaValAsnIleSerAlaAsnGlyPheGlyPheAlaIleCys 1238
Db 3955 TTGCCAGAGCTGCTGGGAATACAGCATGAAAGTGAAGTGAAGAGATGTGTCTACTCCTC 4014
Qy 1239 GlnLeuAsnValValTyrAsnValLysAlaSerGlySerSerArgArgArgSerIle 1258
Db 4015 CAGACATCTTGAATACAAATATT-----CTC 4041
Qy 1259 GlnAsnGlnGluAlaPheAspLeuAspValAlaValLys-----GluAsnLysAsp 1275

Qy	352	GluPheAspTyrThrThrValLeuLysProSerLeuAsnPhetThrAlaThrValLys	371
Db	1133	CCCTTCCTGGG-----CAG	1147
Qy	372	ValThrArgAlaAspGlyAsnGlnLeuThrLeuGluArgAsnAsnValValIle	391
Db	1148	GTGGCCCTAGTAGATGGGAAGGCCCTCCCTATACCA-----AATAAGTCATA	1195
Qy	392	ThrValThrGlnArgAsnTyrThrGluTyrTrpSerGlySerAsnSerGlyAsnGlnLys	411
Db	1196	TTCATC--AGAGGAATGAAGCAAACTATATAC-----TCCAATGCTACACGGATGAG	1246
Qy	412	MetGluAlaValGln--LysIleAsnTyrThr-----ValProGlnSerGlyThrPhe	428
Db	1247	CATGGCCTGTACAGTTCTCTATCAACACCAACCACTATGGTACTCTCTTACTGTT	1306
Qy	429	LysIleGluPhePro-----IleLeuGluAspSer	438
Db	1307	AGGCTCAATTACAAGATCGTAGTCCCTGTACGGCTACCAGTGGGTGCAGAGAACAC	1366
Qy	439	SerGluLeuGlnLeuLysAlaTyrPheLeuGlySerLysSerMetAlaValHisSer	458
Db	1367	GAAGAGGCACATCACACTGCTTAT-----	1390
Qy	459	LeuPheLysSerProSerLysThrTyrIleGlnLeuLysThrArgAspGluAsnIleLys	478
Db	1391	CTTGTGTCTCCCAAGCAAGAGCTTTGTCCACCTTGAGGCCCATGTCTCATGAACATACC	1450
Qy	479	ValGlySer-----ProPheGluLeuValValSerGlyAsnLys-----Arg	492
Db	1451	TGTGGCCCATCTACAGACGTCCAGGCACATTATATCTGAATGGAGGCCACCTCTGCGGG	1510
Qy	493	LeuLysGluLeuSer-----TyrMetValValSerArgGlyGlnLeuValAlaValGly	510
Db	1511	CTGAAGAAGCTCTCCTTTTATTATCTGATAATGGCAAGGAGGCAATGTCCGAACCTGGG	1570
Qy	511	-----LysGlnAsnSerThr-----MetPheSerLeuThr	520
Db	1571	ACTCATGGACTGTGTGAACAGCAGGAAGCATGAAGGCCCATTTTCCATCTCAATCCCT	1630
Qy	521	ProGluAsnSerTrpThrProLysAlaCysValIleValTyrTyrIleGluAspAspGly	540
Db	1631	GTGAAGTCAGACATGTCTCTCGCTCGCTGCTCATCTATGCTGTGTTTACCTACCGGG	1690
Qy	541	GluIleLeuSerAspValLeuLysIleProValGlnLeuValPheLysAsnLysIleLys	560
Db	1691	GACCTGATTGGGGATTCTCGAAAAATATGATGTTGAAAATTGTCTGGGCCAACAAAGGTGGAT	1750
Qy	561	LeuTyrTrpSerLysValLysAlaGluProSerGluLysValSerLeuArgIleSerVal	580
Db	1751	TTGAGCTTCAGCCCATCACAAGTCTCCAGCCTCACGCCACCTGCCAGTCACAGCG	1810
Qy	581	ThrGlnProAspSerIleValGlyIleValAlaValAspLysSerValAsnLeuMetAsn	600
Db	1811	GCT--CCTCAGTCCGTCTGGCCCTCGTGTCTGGACCAAAAGCGTGTCTCATGAAG	1867
Qy	601	AlaSerAsnAspIleThrMetGluAsnValValHisGluLeu--GluLeuTyrAsnThr	619
Db	1868	CCTGATGCTGAGCTCTCGGCGTCTCGGTATACAACTGCTTACAGAAAAGGACCTCCT	1927
Qy	620	GlyTyr-----TyrLeuGlyMet	635
Db	1928	GGCTTCCTCGGCCCTTTGAATGACAGGACGATGAAGACTGCATCAATCGTCATAATGTC	1987
Qy	626	PheMetAsnSer-----PheAla	631
Db	1988	TATATTATATGAATACATATATCTCCAGTATCAAGTACAAATGAAAAGGATATGTACAGC	2047
Qy	632	ValPheGlnGluCysGlyLeuTyrValLeuThrAspAlaLeuLeuThrLysAspTyrIle	651
Db	2048	TTCCTAGGACATGGGCTTAAAGGCATTACCAACCTCAAAGATTCGTAATCCCAAAATG	2107

Qy	652	AspGlyValTyrAspAsnAlaGlu		----	Tyr	660
Db	2108	TGTCACAGCTTCAACAGATGATAAAATGCATGACCTGAAGGCTACGTGTAGGTAGTTTTAT				2167
Qy	661	AlaGluArgPheMetGluGluAsnGluGlyHisIleValAspIleHisAspPheSerLeu				680
Db	2168	GAGTCAGATGTAATGGGAAGAGCCATGACGCCCTGGTGCATGTTCAAGAG				2218
Qy	681	GlySerSerProHis	-----	ValaGlyHisPheProGluThrTrpIleThrLeu	697	
Db	2219	-----CCTCACACGGAGACCGTACGAAAGTACTTCCTCAGACATGGATCTCGGAT				2269
Qy	698	AspThrAsnMetGlyTyrArgIleTyrGlnGluPheGluValThrValProAspSerIle				717
Db	2270	TTGGTGGGTAAACTACGACGGGGTGGTAGGTAGGATAACAGTCCCTGACACATC				2329
Qy	718	ThrSerTrpValAlaThrGlyPheValIleSerGluAspLeuGlyLeuGlyLeuThrThr	737			
Db	2330	ACCGAGTGGAAAGCGGGGCCCTTCGCTGTCGTGAAGATGCTGCATGTAATCTCTTCC	2389			
Qy	738	ThrProValGluLeuGlnAlaPheGlnProPhePheIlePheLeuAsnLeuProTyrSer	757			
Db	2390	ACT---GCCCTCTCCGAGCCTTCCAGCCCTCTTTGTGGAGCTTACAATGCCTTACTCT	2446			
Qy	758	ValIleArgGlyGluGluPheAlaLeuGluIleThrIlePheAsnTyrLeuIysAspAla	777			
Db	2447	GTGATTCGTGGAGAGCCCTTCACACTCAAGCCACCGTCTTAACCTTCCCAATGC	2506			
Qy	778	ThrGluValIysValIleIleGluIysSerAspIysPheAspIleuMetThrSerSer	797			
Db	2507	ATCCGGTCTCAGTGTGACGTGGGAAGCCTCTCCCGCCTTCCTGCTGCTCCAGTGGAGAAG	2566			
Qy	798	Glu	-----	IleAsnAlaThrGlyHisGlnGlnThrLeuLeuValProSer	812	
Db	2567	GAACAAGCGCTCACTGCATCTGTGMAACGGGGCGCA	-----	-----	2605	
Qy	813	GluAspGlyAlaThrValLeuPheProIleArgProThrHisLeuGlyGluIleProIle	832			
Db	2606	-----ACTGTGCTCGGCAGTAACCCCAAGTCACTAGGAATGTGAATTTTC	2653			
Qy	833	ThrValThrAlaLeuSer	-----	-----	ProThrAla	841
Db	2654	ACTGTAGCGCAGGACGACTAGAGTCTCAAGAGCTGTGCGGACTGAGTGCCTTCAGTT	2713			
Qy	842	-----SerAspAlaValThrGlnMetIleLeuValIysAlaGluGlyIle	856			
Db	2714	CCTGAACACGGAAGAAAGACACAGTCAATCAAGCCTCTGTGTGTTGAACCTGAAGACTA	2773			
Qy	857	GluIysSerTyrSerGlnSerIleLeuLeuAspLeuThrAspAsnArgLeuGlnSerThr	876			
Db	2774	GAGAAGAAACAACATTCACCTCCCTACTTTGTCATCAGGTGGTGAGGTTTCT	2827			
Qy	877	LeuIysThrLeuSerPheSerPheProAsnThrValThrGlySerGluArgValGln	896			
Db	2828	---GAAGAAATATCCCTGAACCTGCCACCAAAATGTGTTAGAAGAACTGCGCCGCTTCT	2884			
Qy	897	IleThrAlaIleGlyAspValLeuGlyProSerIleAsnGlyLeuAlaSerLeuIleArg	916			
Db	2885	GTCTCAGTTTTGGGAGACATATTAGGCTCTGCGCCACAAACACACAAAATCTCTCCAG	2944			
Qy	917	MetProTyrGlyCysGlyGluGlnAsnMetIleAsnPheAlaProAsnIleTyrIleLeu	936			
Db	2945	ATGCCCTATGGCTGTGGAGAGCGAATATGGTCTCTTCTCTTAACATCTATGACTG	3004			
Qy	937	AspTyrLeuThrIysIysIysGlnLeuThrAspAsnLeuIysGlnIysAlaLeuSerPhe	956			
Db	3005	GAATTATCTAAATGAACACACAGCCTTACTCCAGAGATCAAGTCCAAGGCCATTTGGCTAT	3064			
Qy	957	MetArgGlnGlyTyrGlnArgGluLeuLeuTyrGlnAlaArgGluAspGlySerPheSerAla	976			
Db	3065	CTCAACTGTTTACCAAGACACAGTGTGAACATAACAACACTATGATGGCTCTACAGCACC	3124			
Qy	977	PheGly---AsnTyrAspProSer---GlySerThrTrpLeuSerAlaPheValLeuArg	994			

Db 3125 TTGGGAGGATATGCGAGAACAGGCAACACCTGGCTCACAGCCTTTGTTCTGAAG 3184
Qy 995 CysPheLeuGluAlaValProTyrIleAspIleAspGlnAsnValLeuHisArgThrTyr 1014
Db 3185 ACTTTTCCCAAGCTCGAGCTCATCTTTCATGATGAGCAACACATTACCCAGCCCTC 3244
Qy 1015 ThrTriLeuLysGlyHisGlnLysSerAsnGlyGluPheTrpAspProGlyArgValIle 1034
Db 3245 ATATGGCTCTCCAGAGGCAAGGACAATGGCTTTTCAGGAGCTCTGGGTCACTGCTC 3304
Qy 1035 HisSerGluLeuGlnGlyGlyAsnLysSerProValThrLeuThrAlaTyrIleValThr 1054
Db 3305 AACAAATGCCATAAAGGAGAGTAGAAGATGAAGTGAACCTCTCCGCTTATATCACCATC 3364
Qy 1055 SerLeuLeuGlyTyrArgLysTyrGlnProAsnIleAspValGlnGluSerIleHisPhe 1074
Db 3365 GCCCTTCTGGAGATTCCTCTCACAGTCACCTCACCTGTTGTCGCAATGCCCTGTTTGC 3424
Qy 1075 LeuGluSer-----GluPheSerArgGlyIleSerAspAsnTyrThr 1088
Db 3425 CTGGAGTCAGCCTGGAAGACAGACAGCAAGAGGGGACCATGSC---AGCCATGTATATACC 3481
Qy 1089 LeuAlaLeuIleThrTyrAlaLeuSerSerValGlySer---ProLysAlaLysGluAla 1107
Db 3482 AAGCACTGTGGCTATGCTTTTGGCTCGAGGTAAACAGGACAGAGGAAGGAAGTA 3541
Qy 1108 LeuAsnMetLeuThrTrpArgAlaGluGlnGluGlyMetGlnPheTrp----- 1124
Db 3542 CTCAAAGTCACTTAATGAGGAAGCTGTGAAGAAAGACAACTCTGTCCATTGGGAGCCCT 3601
Qy 1125 ValSerSerGluSerLysLeuSerAspSerTrpGlnProArg-----SerLeuAspIle 1142
Db 3602 CAGAAACCCAGGACAGGCTGGGGCATTTTTACGAACCCAGGCTCCCTCTGTGAGGTG 3661
Qy 1143 GluValAlaAlaTyrAlaLeuLeuSerHisPheLeuGlnPheGln-----ThrSer 1159
Db 3662 GAGATGACATCCATGTGCTCTCGCT--TATCTACGCCCCAGCCAGCCCAACTCG 3718
Qy 1160 GluGlyIlePro-----IleMetArgTrpLeuSerArgGlnArgAsnSerLeu 1175
Db 3719 GAGGACCTGACCTCTGCAACCAACATCGTAAGTGGATCAGGAAGCAGCAATGCCCCAG 3778
Qy 1176 GlyGlyPheAlaSerThrGlnAspThrValAlaLeuLysAlaLeuSerGluPheAla 1195
Db 3779 GCGGTTTCTCCCAACCCAGGACAGAGTGCTGCTCATGCTCTGTCAAATATGGA 3838
Qy 1196 AlaLeuMetAsnThrGluArgThrAsnIleGlnValThrValThrGlyProSerSerPro 1215
Db 3839 GCGCCACATTAC---AGGACTGGGAAGGCTGCACAGGTGACTATCCAGTCTTCAGGG 3895
Qy 1216 SerProLeuAlaValValGln----- 1222
Db 3896 ACATTTTCCAGCAATTTCCAAAGTGGCAACAACAATGCGCTGTACTGCGAGAGGTCTCA 3955
Qy 1223 -----ProMetAlaValAsnIleSerAlaAsnGlyPheGlyPheAlaIleCys 1238
Db 3956 TTGCCAGAGCTGCTGGGGAATACAGCATGAAGTGACAGAGAGGATGTGCTACCTC 4015
Qy 1239 GlnLeuAsnValValTyrAsnValLysAlaSerGlySerSerArgArgArgSerIle 1258
Db 4016 CAGACCTCTTGAATAACAATATT-----CTC 4042
Qy 1259 GlnAsnGlnGluAlaPheAspLeuAspValAlaValLys-----GluAsnLysAsp 1275
Db 4043 CCAGAAAGGAAGAGTTCCCTTTGCTTTAGGAGTGCAGACTCTGCTCNAATCTTGAT 4102
Qy 1276 AspLeuAsn---HisValAspLeuAsnValCysThrSerPheSerGlyProGly----- 1292
Db 4103 GAACCCAAAGCCACACACAGCTTCCAAATCTCCCTAAGTGTCACTTACACAGGAGCGC 4162
Qy 1293 ---ArgSerGlyMetAlaLeuMetGluValAsnLeuLeuSerGlyPheMetValProSer 1311

Db 4163 TCTGCTCCACATGCGCATGCTTGTGATGGAAGTGGTCTCTGGCTTCATTCCCTGAAG 4222
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Db 4223 CCAACAGTGAATAATCTTGAAGAATCTAACCATGTGACCGCAGACAGTACAGCAGCAC 4282
Qy 1329 LysLeuAsnLeuTyrLeuAspSerValAsnGlnThrGlnPheCysValAsnIleProAla 1348
Db 4283 CATGTCTTGATTTACCTTTGATAAAGGTGCAAAATCAGACACTGAGCTTCTTTCACGGTT 4342
Qy 1349 ValArgAsnPheLysValSerAsnThrGlnAspAlaSerValSerIleValAspTyrTyr 1368
Db 4343 CTGCAAGATGTCCTCAGTAGAGATCTCAACAGCAGCATAGTGAAGTCTATGATTACTAC 4402
Qy 1369 GluProArgArgGlnAlaValArgSerTyrAsnSer 1380
Db 4403 GAGACGGATGAGTTTGCATCGCTGAGTACAATGCT 4438
RESULT 13
US-10-116-802-21
; Sequence 21, Application US/10116802
; Publication No. US20030065157A1
; GENERAL INFORMATION:
; APPLICANT: Amy Lasek
; TITLE OF INVENTION: GENES EXPRESSED IN LUNG CANCER
; FILE REFERENCE: PA-0045 US
; CURRENT APPLICATION NUMBER: US/10/116,802
; PRIOR FILING DATE: 2002-04-04
; PRIOR APPLICATION NUMBER: 60/281,593
; PRIOR FILING DATE: 2001-04-04
; NUMBER OF SEQ ID NOS: 519
; SOFTWARE: PERL Program
; SEQ ID NO 21
; LENGTH: 4769
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: misc feature
; OTHER INFORMATION: Incyte ID No: 273154CB1
US-10-116-802-21
Alignment Scores:
Pred. No.: 6,6e-134 Length: 4769
Score: 1441.00 Matches: 451
Percent Similarity: 46.20% Conservative: 266
Best Local Similarity: 29.08% Mismatches: 551
Query Match: 19.61% Indels: 284
DB: 13 Gaps: 59
US-10-020-095-4 (1-1428) x US-10-116-802-21 (1-4769)
Qy 12 LeuLeuCysValCysThrAlaAlaLeuAlaValAlaProGlyProArgPheLeuValThr 31
Db 279 CTCCTTGGTCTCTCCGCCACAGACGCTCAGTCTCTGGAAACCCGAGTATATGTTCTG 338
Qy 32 AlaProGlyIleIleArgProGlyGlyAsnValThrIleGlyValGluLeuLeuGluHis 51
Db 339 GTCCCTCCCTGCTCCACACT--GAGACCACCTGAGAAGGCTGTGCTCTTCTGAGCTAC 395
Qy 52 CysProSerGlnValThrValLysAlaGluLeuLeuLysThrAlaSerAsnLeuThrVal 71
Db 396 CTGAATGACACACTGACTGTAAGTCTTCTTGGAGTCTGTGAGGGGAAACAGGAGCCTC 455
Qy 72 ---SerValLeuGluAlaGluGly---ValPheGluLysGlySerPheLysThrLeuThr 89
Db 456 TTCATGTACCTGGAGCGGAGAAATGACGTACTCCACTGTGCGCTTC----- 503
Qy 90 LeuProSerLeuProLeuAsnSerAlaAspGlu-----IleTyrGluLeuArgVal 106
Db 504 -----GCTGTGCCAAAGTCTTCAATCAATGAGGAGGTAATGTTCTCTCACTGTCACAGTG 557
Qy 107 ThrGlyArgThrGlnAspGluLeuLeuPheSerAsnSerThrArgLeuSerPheLeuThr 126

558	DB	AAAGGACCAACCCCAAGAA-----TTTAAAGAAGCGGACCAACAGTGTGGTTAAGAAC	608
127	QY	LysArgIleSerValPheIleGlnThrAspLysAlaLeuTyrLysProLysGlnGluVal	146
609	DB	CGAGCAGCTCTGGCTTTGTCCAGACAGACAAATCAATCTACAAACCAGGCGACAGACGTG	668
147	QY	LysPheArgIleValThrLeuPheSerAspPheLysProTyrLysThrSerLeuAsnIle	166
669	DB	AAATTTCTGTGTCTCCATCGATGAAAACTTCCACCCCTGGAATGAGTTGATTCACATA	728
167	QY	Leu--LleLysAspProLysSerAsnLeuIleGlnGlnThrLeuSerGlnGlnSerAsp	185
729	DB	GTATACATTACAGATCCCAAGGAAATCGCATCGCAATGGCAGAGTTTCCAGTTAGAG	788
186	QY	LeuGlyValIleSerLysThrPheGlnLeuSerSerHisProIleLeuGlyAspTrpSer	205
789	DB	GGTGGCCTCAAGCAATTTCTTTTCCCTCTCATCAGAGCCCTTCCAGGCGCTCTACAAG	848
206	QY	IleGlnValGlnValAsnAsp-----GlnThrTyrTyrGlnSerPheGlnValSerGlu	223
849	DB	GTGTGTGTACAGAAGAAATCAGGTGGAGGACAGACAC---CCTTTACCGTGGAGGAA	905
224	QY	TyrValLeuProLysPheGluValThrLeuGlnThrProLeuTyrCysSerMetAsnSer	243
906	DB	TTTGTCTCTCCAAAGTTTGAAGTACAAGTACAGTGGCCAAAGATAATCAACCATCTTGGAA	965
244	QY	LysHisLeuAsnGlyThrIleThrAlaLysTyrThrTyrGlyLysProValLysGlyAsp	263
966	DB	GAGAGATGAATGATCATCGTGTGGCCTATACACATATGGGAAGCCTGTCCTGGACAT	1025
264	QY	ValThrLeuThrPheLeuProLeu-----	271
1026	DB	GTGACTGTGACCAITTCAGAAAGTATAGTCAGCTTCCGACTGCCACGGTGAAGATTCA	1085
272	QY	-----	276
1086	DB	CAGGCTTTCTGTGAAATTCAGTGGACAGCTAAACGCCATGGCTCTCTATCAGCAA	1145
277	QY	LysLysAsnIleThrLysThrPheLysIleAsnGlySerAlaAsnPheSerPheAsnAsp	296
1146	DB	GTAAAA-----ACCAAGTCTTCCAGCTGAAGAG-----AAGGAG	1181
297	QY	GluGluMetLysAsnValMetAspSerSerAsnGlyLeuSerGluTyrLeuAspLeuSer	316
1182	DB	TATGAATGAA-----CTTCACACTGAGGCCACAGATCCAA	1217
317	QY	SerProGlyProValGluIleLeuThr-----ThrValThrGluSerVal	331
1218	DB	GAAGAAGAACAGTGGTGGAAATTCATCGAAGCGAGTCCAGTGAATTCACAGAACCATTA	1277
332	QY	ThrGlyIleSerArgAsnValSerThrAsnValPhePheLysGlnHisAspTyrIleIle	351
1278	DB	ACCAAACTCTCA---TTTGTGAAGTGGACTCACACITTCGACAGGGA-----ATT	1325
352	QY	GluPhePheAspTyrThrThrValLeuLysProSerLeuAsnPheThrAlaThrValLys	371
1326	DB	CCCTTCTTTGGG-----	1340
372	QY	ValThrArgAlaAspGlyAsnGlnLeuThrLeuGluIleArgAsnAsnValIle	391
1341	DB	GTGGCCTAGTAGATGGAAAGGCGTCCCTATACCA-----AATAAGTCATA	1388
392	QY	ThrValThrGlnArgAsnTyrThrGluTyrTrpSerGlySerAsnSerGlyAsnGlnLys	411
1389	DB	TTTCATC---AGAGGAAATGAAGCAAACTATTAC-----TCCAATGCTACCCAGGATGAG	1439
412	QY	MetGluAlaValGln---LysIleAsnTyrThr-----ValProGlnSerGlyThrPhe	428
1440	DB	CATGGCCTTTGACAGTCTCTATACACACCAACCAATGTTATGGGTACCTCTCTTACTGTT	1499
429	QY	LysIleGluPhePro-----IleLeuGluAspSer	438
1500	DB	AGGCTCAATTACAAGGATCGTAGTCCCTGTTATACGGCTACCAAGTGGGTGCAGAGAACAC	1559

Qy	439	SerGlnLeuGlnLeuLysAlaTyrPheLeuGlySerLysSerSerMetAlaValHisSer	458
Db	1560	GAAGAGGCACATCACACTGCTTAT	1583
Qy	459	LeuPheLysSerProSerLysThrTyrIleGlnLeuLysThrArgAspGluAsnIleLys	478
Db	1584	CTTGTGTTCTCCCNAGCAGAGCTTGTCCACCTTGAGCCCATGTCTCATGAACATACCC	1643
Qy	479	ValGlySer	492
Db	1644	TGTGGCCATACTCAGACAGTCACAGGCACATTAATTCGAATGAGGAGCCACCTGTCTGGGG	1703
Qy	493	LeuLysGlnLeuSer	510
Db	1704	CTGAGAGAGCTCTCTCTTATTATCTGATAATGGCAAGGAGGCATTGTCCGAAGCTGG	1763
Qy	511	LysGlnAsnSerThr	520
Db	1764	ACTCATGGACTGCTGTGAAGCAGGAGACATGAAGGGCCATTTTCCATCTCAATCCCT	1823
Qy	521	ProGluAsnSerTrpThrProLysAlaCysValIleValTyrTyrIleGluAspAspGly	540
Db	1824	GTGAGTCAGACATTGCTCTCTGCTCGTGTGCTCATCTATGCTGTTTACCTACCGGG	1883
Qy	541	GluIleIleSerAspValLeuLysIleProValGlnLeuValPheLysAsnIleLys	560
Db	1884	GAGCTGATTGGGATTCTGCAAAATATGATGTGAAATTTGCTGGCCCAACAAGGTGGAT	1943
Qy	561	LeuTyrTrpSerLysValLysAlaGluProSerGluLysValSerLeuArgIleSerVal	580
Db	1944	TTGAGCTTCAGCCCATCACAAAGCTCTCCAGCCTCACAGCCACCTGCGAGTCACAGCG	2003
Qy	581	ThrGlnProAspSerIleValGlyIleValAlaValAspLysSerValAsnLeuMetAsn	600
Db	2004	GCT---CCTCAGTCCGCTGTCGGCCTCCGCTGCTGGACCAAGCGTGTGCTCATGAAG	2060
Qy	601	AlaSerAsnAspIleThrMetGluAsnValValHisGlnLeu	619
Db	2061	CCTGATGCTGAGCTCTGGGCTCTCGGTTTACAACTGTCTACAGAAAAAGGACCTCACT	2120
Qy	620	GlyTyr	625
Db	2121	GGCTTCCTCGGCTTTGAATGACCAGGACGATGAAGACTGCATCAATGCTCATATGTC	2180
Qy	626	PheMetAsnSer	631
Db	2181	TATATTAAATGGAATCACATATATCTCCAGTATCAAGTACAAATGAAAGGATATGTACAGC	2240
Qy	632	ValPheGlnCysGlyLeuTrpValLeuThrAspAlaAsnLeuThrLysAspTyrIle	651
Db	2241	TTCTAGGACATGGCTTTAAAGGCATTACCAACTCAAAGATTCTGAACCCCAAAATG	2300
Qy	652	AspGlyValTyrAspAsnAlaGlu	660
Db	2301	TGTCACAGCTTCAACAGTATGAATTCATGTCAGCTGAGGCTACGTGTAGGTTTTAT	2360
Qy	661	AlaGluArgPheMetGluGluAsnGluGlyHisIleValAspIleHisAspPheSerLeu	680
Db	2361	GAGTCAGATGAATGGGAAGAGGCCCATGACGCTGTGTGATGTTGAAAG	2411
Qy	681	GlySerSerProHis	697
Db	2412	-----CCTCACACGGAGACCGTACGAAAGTACTTCTCTGAGACATGGATCTGGAT	2462
Qy	698	AspThrAsnMetGlyTyrArgIleTyrGlnGluPheGluValThrValProAspSerIle	717
Db	2463	TTGGTGGTGAATCACTCAGCAGGTGTGGCTGAGGTAGGATACAGTCTCTGACCAATC	2522
Qy	718	ThrSerTrpValAlaThrGlyPheValIleSerGluAspLeuGlyLeuGlyLeuThrThr	737
Db	2523	ACCGAGTGAAGCAGCGGGCTTCTGCCTGTCTGAAGATGCTGCATGGATCTCTCTCC	2582

738 ThrProValGluLeuGlnAlaPheGlnProPhePheIlePheLeuAsnLeuProTyrSer 757
Db ACT---GCCCTCTCCGAGCCTTCACGCCCTCTTTGTGGAGTGCACAATCGCTACTCT 2639

758 ValIleArgGlyGluGluPheAlaLeuGluIleThrIlePheAsnTyrLeuLysAspAla 777
Db ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| 2640

778 ThrGluValLysValIleIleGluLysSerAspLysPheAspIleLeuMetThrSerSer 797
Db ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| 2700

798 Glu-----IleAsnAlaThrGlyHisGlnGlnThrLeuLeuValProSer 812
Db GAACAAGCGCTCACTCATCTGTGCAAACGGCGGCAAA----- 2760

813 GluAspGlyAlaThrValLeuPheProIleArgProThrHisLeuGlyGluIleProIle 832
Db ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| 2799

833 ThrValThrAlaLeuSer-----ProThrAla 841
Db ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| 2847

842 -----SerAspAlaValThrGlnMetIleLeuValLysAlaGluGlyIle 856
Db CCTCAACACGAAGAAAGACACAGTCATCAAGCCTCTGTGGTGTAACCTGAAGACTA 2966

857 GluLysSerTyrSerGlnSerIleLeuLeuAspLeuThrAspAsnArgLeuGlnSerThr 876
Db ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| 2967

877 LeuLysThrLeuSerPheSerPheProAsnThrValThrGlySerGluArgValGln 896
Db ---GAAGAATTATCCCTGAACCTCCACAAAATGTTGTAGAGNAATCTGCCGAGCTTCT 3077

897 IleThrAlaIleGlyAspValLeuGlyProSerIleAsnGlyLeuAlaSerLeuIleArg 916
Db ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| 3078

917 MetProTyrGlyCysGlyGluGlnAsnMetIleAsnPheAlaProAsnIleTyrIleLeu 936
Db ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| 3138

937 AspTyrLeuThrLysLysLysGlnLeuThrAspAsnLeuLysGluLysAlaLeuSerPhe 956
Db ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| 3198

957 MetArgGlnGlyTyrGlnArgGluLeuLeuTyrGlnArgGluAspGlySerPheSerAla 976
Db ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| 3258

977 PheGly--AsnTyrAspProSer--GlySerThrTrpLeuSerAlaPheValLeuArg 994
Db ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| 3318

995 CysPheLeuGluAlaAspProTyrIleAspIleAspGlnAsnValLeuHisArgThrTyr 1014
Db ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| 3378

1015 ThrTrpLeuLysGlyHisGlnLysSerAsnGlyGluPheTrpAspProGlyArgValIle 1034
Db ATATGGCTCTCCCAGAGCAGAGACATGGCTGTTTCAGGAGCTCTGGGTCACTGCTC 3497

1035 HisSerGluLeuGlnGlyGlyAsnLysSerProValThrLeuThrAlaTyrIleValThr 1054
Db ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| 3498

1055 SerLeuLeuGlyTyrArgLysTyrGlnProAsnIleAspValGlnGluSerIleHisPhe 1074
Db ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| 3558

1075 LeuGluSer-----GluPheSerArgGlyIleSerAspAsnTyrThr 1088

3618	Db		CTGGAGTCAGCCCTGGAGACAGCAGCAAGAAGGGACCATTGGC---AGCCATGTATATATACC	3674
1089	Qy		LeuAlaLeuIleThrTyRAlaLeuSerSerValGlySer---ProLysAlaLysGluAla	1107
3675	Db		AAAGCACTGCGCCCTATGCTTTTGCCCTGGCAGGTAACACGAGCAGAGGAAGGAAGTA	3734
1108	Qy		LeuAsnMetLeuThrTrpArgAlaGluGlnGluGlyGlyMetGlnPheTrp-----	1124
3735	Db		CTCAAGTCATCTAATGAGGAAGCTGTGAAGAAACAACACTCTGTCCATTGGGAGCGCCCT	3794
1125	Qy		ValSerSerGluSerLysLeuSerAspSerTrpGlnProArg-----SerLeuAspIle	1142
3795	Db		CAGAAACCCAGGCACACAGTGGGCATTTTACGACCCAGCTCCCTCTGCTGAGGTG	3854
1143	Qy		GluValAlaAlaTyRAlaLeuLeuSerHisPheLeuGlnPheGln-----ThrSer	1159
3855	Db		GAGATGACATCTATGTGCTCCTCGCT---TATCTCAGCGCCAGCGACGCCCAACCTCG	3911
1160	Qy		GluGlyIlePro-----IleMetArgTrpLeuSerArgGlnAsgAsnSerLeu	1175
3912	Db		GAGACCTGACCTCTGCACCAACATCGTGAAGTGATCAGGAAGCAGAGATGCCAG	3971
1176	Qy		GlyGlyPheAlaSerThrGlnAspThrValAlaLeuLysAlaLeuSerGluPheAla	1195
3972	Db		GGCGGTTTCCTCCACCCAGGACACAGTGGTGGCTCTCCATGCTCTGTCCAAATATGGA	4031
1196	Qy		AlaLeuMetAsnThrGluArgThrAsnIleGlnValThrValThrGlyProSerSerPro	1215
4032	Db		GCAGCCACATTACC---AGACCTGGGAAGCTGCACAGGTGACTATCCAGTCTTCAGGG	4088
1216	Qy		SerProLeuAlaValValGln-----	1222
4089	Db		ACATTTTCCAGCAAAATCCAAGTGGCAACAACACCCCTGTTACTGCGACAGGTCTCA	4148
1223	Qy		-----ProMetAlaValAsnIleSerAlaAsnGlyPheGlyPheAlaIleCys	1238
4149	Db		TTCGACAGCTGCTCGGGAAATCAGCATGAAGTGCAGGAGAGGATGTGCTACCTC	4208
1239	Qy		GlnLeuAsnValValTyRAsnValLysAlaSerGlySerSerArgArgArgSerIle	1258
4209	Db		CAGACATCTTGAAATACATATT-----	4235
1259	Qy		GlnAsnGlnGluAlaPheAspLeuAspValAlaValLys-----GluAsnLysAsp	1275
4236	Db		CCGAAAGGAAGAGATTCCCTTGTGTTTAGGAGTGCAGACTGTGCTCAAACTTGTGAT	4295
1276	Qy		AspLeuAsn---HisValAspLeuAsnValCysThrSerPheSerGlyProGly----	1292
4296	Db		GAACCCAAAGCCACACACCAGCTTCCAAATCTCCCTAAGTGTGACTACAGGGAGCCGC	4355
1293	Qy		---ArgSerGlyMetAlaLeuMetGluValAsnLeuLeuSerGlyPheMetValProSer	1311
4356	Db		TCTGCCCTCCAAACATGGCGATCGTGTAGTGAAGATGGTCTCTGGCTTCATTCCCTGAAG	4415
1312	Qy		GluAlaIleSerLeu-----SerGluThrValLysLysValGluTyRAspHisGly	1328
4416	Db		CCAACGTGAAATGCTTGAAGATCTAACCATGTGAGCCGGACAGAGTCAGCAGCAAC	4475
1329	Qy		LysLeuAsnIleTyRLeuAspSerValAsnGluThrGlnPheCysValAsnIleProAla	1348
4476	Db		CATGCTCTGATTATACCTTGATTAAGGTGTCAAAATCAGACTGAGCTTGTCTTCAACGTT	4535
1349	Qy		ValArgAsnPheLysValSerAsnThrGlnAspAlaSerValSerIleValAspTyR	1368
4536	Db		CTGCAAGATGCCAGTAAGAGATCTGAACACCCATAGTGAAGTCTATGATTACTAC	4595
1369	Qy		GluProArgGlnAlaValArgSerTyRAsnSer	1380
4596	Db		GAGACGGATGAGTTTGAATTTGCTGAGTACAATGCT	4631

RESULT 14
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Db 910 GTAATA-----ACCAAGGCTCTCCAGCTGAAGAG-----AAGGAG 945
 QY 297 GluGluMetLysAsnValMetAspSerSerAsnGlyLeuSerGluTyrLeuAspLeuSer 316
 Db 946 TATGAATGAAA-----CTTCACACTGAGGCCCGACATCCAA 981
 QY 317 SerProGlyProValGluLeuLeuThr-----ThrValThrGluSerVal 331
 Db 982 GAAGAAGGACAGCTGGTGGNAATGACTGGAGGCGACTCCAGTCAAAATCACAGAACCATTA 1041
 QY 332 ThrGlyLeuSerArgAsnValSerThrAsnValPhePheLysGlnHisAspTyrIleIle 351
 Db 1042 ACCAAACTCTCA---TTTGTAAGTGGACTCACTCTTCGACAGGGA-----ATT 1089
 QY 352 GluPhePheAspTyrThrThrValLeuLysProSerLeuAsnPheThrAlaThrValLys 371
 Db 1090 CCTTCTCTTGGG-----CAG 1104
 QY 372 ValThrArgAlaAspGlyAsnGlnLeuThrLeuGluGluArgAsnAsnValValIle 391
 Db 1105 GTGGCGCTAGTAGTGGAAAGCGCTCCCTATACCA-----AATAAAGTCATA 1152
 QY 392 ThrValThrClnArgAsnTyrThrGluTyrTrpSerGlySerAsnSerGlyAsnGlnLys 411
 Db 1153 TTCATC---AGAGGAATGAAGCAAACTATTAC-----TCCAATGCTACCCAGGATGAG 1203
 QY 412 MetGluAlaValGln---LysIleAsnTyrThr-----ValProGlnSerGlyThrPhe 428
 Db 1204 CATGGCGCTGTACAGTCTCTATACACACCACCAAGCTTATGGTACCTCTCTTACTGTT 1263
 QY 429 LysIleGluPhePro-----IleLeuGluAspSer 438
 Db 1264 AGGGTCAATTACAAAGGATCGTAGTCCCTGTGTACGGCTACAGTGGGTGTCAGAAAGAACAC 1323
 QY 439 SerGluLeuGlnLeuLysAlaTyrPheLeuGlySerLysSerMetAlaValHisSer 458
 Db 1324 GAAGAGCACATCACACTGCTTAT----- 1347
 QY 459 LeuPheLysSerProSerLysThrTyrIleGlnLeuLysThrArgAspGluAsnIleLys 478
 Db 1348 CTTGTGTCTCCCAAGCAAGAGCTTGTCCACCTTGAGGCCATGTCTCATGAACATACCC 1407
 QY 479 ValGlySer-----ProPheGluLeuValValSerGlyAsnLys-----Arg 492
 Db 1408 TGTGGCCATCTCAGACAGTCCAGGCACATTAATTCTGAATGGAGGCGCCCTGTGGGG 1467
 QY 493 LeuLysGluLeuSer-----TyrMetValValSerArgGlyGlnLeuValAlaValGly 510
 Db 1468 CTGAAGAAGCTCTCCTTTTATTATCTGATAATGCAAGGAGGCGCATTTGCCGAACCTGG 1527
 QY 511 -----LysGlnAsnSerThr-----MetPheSerLeuThr 520
 Db 1528 ACTCATGGACTGTGTGAAGCAGCAAGACATGAAGGGCCATTTTCCATCTCAATCCCT 1587
 QY 521 ProGluAsnSerTrpThrProLysAlaCysValIleValTyrTyrIleGluAspAspGly 540
 Db 1588 GTGAAGTCACACATGCTCTGTCTGTGGTCTCATCTATCTGCTGTCTTACCTACCGGG 1647
 QY 541 GluIleLeuSerAspValLeuLysIleProValGlnLeuValPheLysAsnLysIleLys 560
 Db 1648 GACGTGATTGGGATTCTGCAAAATATGATGTTGAAAATTTGTCTGGCCCAAGGTGGAT 1707
 QY 561 LeuTyrTrpSerLysValLysAlaGluProSerGluLysValSerLeuArgIleSerVal 580
 Db 1708 TTGAGCTTTCAGCCCATCACAAAGTCTCCAGCCTCACAGCCCCACCTGGCAGTTCACAGCG 1767
 QY 581 ThrGlnProAspSerIleValGlyIleValAlaValAspLysSerValAsnLeuMetAsn 600
 Db 1768 GCT---CCTCAGTCCGTCGCGCTCGGTGTGGACCAAGCGTGTGCTCATGAAG 1824
 QY 601 AlaSerAsnAspIleThrMetGluAsnValValHisGluLeu---GluLeuTyrAsnThr 619
 Db 1825 CCTGATGCTGAGCTCTCGGGCTCTCGGTTTACACCTGCTACCAAGAAAGGACCTCACT 1884

QY 620 GlyTyr-----TyrLeuGlyMet 625
 Db 1885 GGCITTCCTCGGCCCTTGAATGATGACGAGCAGATGAGACTCCATCAATCGTCATAATGTC 1944
 QY 626 PheMetAsnSer-----PheAla 631
 Db 1945 TATATTAATGGAATCACATATACTCCAGTATCAAGTACAAATGAAAGGATATGTACAGC 2004
 QY 632 ValPheGlnGluCysGlyLeuTrpValLeuThrAspAlaAsnLeuThrLysAspTyrIle 651
 Db 2005 TTCCTAGAGGACATGGGCTTAAAGGCATTCACCAACTCAAAGATTTCGTAACCCCAATG 2064
 QY 652 AspGlyValTyrAspAsnAlaGlu-----Tyr 660
 Db 2065 TGTCCACAGCTTCAACAGTATGAATGCATGCATGCAGCTGAAGCTCTACGTGAGGTTTTAT 2124
 QY 661 AlaGluArgPheMetGluGluAsnGluGlyHisIleValAspIleHisAspPheSerLeu 680
 Db 2125 GAGTCAGATGTAATGGGAAGAGGCGCATGCACGCTGTGTGCATGTTGAAGAG----- 2175
 QY 681 GlySerSerProHis-----ValArgLysHisPheProGluThrTrpIleTrpLeu 697
 Db 2176 -----CCTCACAGGAGACCGTACAAAGTACTTCCCTGAGACATGGATCTGGAT 2226
 QY 698 AspThrAsnMetGlyTyrArgIleTyrGlnGluPheGluValThrValProAspSerIle 717
 Db 2227 TTGGTGGTGTAAACTCAGCAGGGGTGGCTGAGGTAGGAGTAACAGTCCCTGACACCATC 2286
 QY 718 ThrSerTrpValAlaThrGlyPheValIleSerGluAspLeuGlyLeuGlyLeuThrThr 737
 Db 2287 ACCGAGTGGAGGAGGCGGCTTCTGCTGTCTGAAGATGCTGAGTGGTATCTCTTCC 2346
 QY 738 ThrProValGluLeuGlnAlaPheGlnProPhePheIlePheLeuAsnLeuProTyrSer 757
 Db 2347 ACT---GCCTCTCCGAGCCTTCCAGCCCTCTTTGTGGAGCTTACATGCTTACTCT 2403
 QY 758 ValIleArgGlyGluGluPheAlaLeuGluIleThrIlePheAsnTyrLeuLysAspAla 777
 Db 2404 GTGATTCGTGGAGAGGCCCTTCACACTCAAGGCCAGGCTCTTAAACTACCTTCCCAATGTC 2463
 QY 778 ThrGluValLysValIleLeuLysSerAspLysPheAspIleLeuMetThrSerSer 797
 Db 2464 ATCCGGTCACTGTGACGTGAGCCTTCCGCCCTTCTTGTGCTGCCAGTGGAGAG 2523
 QY 798 Glu-----IleAsnAlaThrGlyHisGlnGlnThrLeuLeuValProSer 812
 Db 2524 GAACAAGCGCCTCACTGCATCTGTGCAAAACGGCGGCAA----- 2562
 QY 813 GluAspGlyAlaThrValLeuPhePheProIleArgProThrHisLeuGlyGluIleProIle 832
 Db 2563 -----ACTGTCTCTGGCGAGTAACCCCAAGTCATTAGGAATGTGAATTC 2610
 QY 833 ThrValThrAlaLeuSer-----ProThrAla 841
 Db 2611 ACTGTGAGCGCAGAGGCGACTAGAGTCAAGAGCTGTGTGGAGCTGAGGTCCCTTCACTT 2670
 QY 842 -----SerAspAlaValThrGlnMetIleLeuValLysAlaGlyIle 856
 Db 2671 COTGAACACGGAAGAAAGACACAGTCAATCAAGCTCTGTGTTGAACCTGGAAGGACTA 2730
 QY 857 GluLysSerTyrSerGlnSerIleLeuLeuAspLeuThrAspAsnArgLeuGlnSerThr 876
 Db 2731 GAGAAGGAAACAACTTCACTCTTGTCCATCAGGTGGTGGAGTTCT----- 2784
 QY 877 LeuLysThrLeuSerPheSerPheProAsnThrValThrGlySerGluArgValGln 896
 Db 2785 ---GAAGAATTTATCCTGAAACTGCCAAATGTGGTAGAAGAAATCTGCCCGAGCTTCT 2841
 QY 897 IleThrAlaIleGlyAspValLeuGlyProSerIleAsnGlyLeuAlaSerLeuLeuArg 916
 Db 2842 GTCTCAGTTTGGGAGACATATTAGGCTCTCCCATGCAAAACACACAAAATCTTCTCCAG 2901

QY 917 MetProTyrGlyCysGlyGluGlnAsnMetIleAsnPheAlaProAsnIleTyrIleLeu 936
DB 2902 ATGCCCTATGGCTGTGGAGGAGCAATATGGTCTCTTCTCTCAACATCTATGACTG 2961
QY 937 AspTyrLeuThrTyrLysLysGlnLeuThrAspAsnLeuLysGluLysAlaLeuSerPhe 956
DB 2962 GATTATCTAATGAACACACAGCAGCTTACTCCAGAGGTCAAGTCCAAGGCCATTGGCTAT 3021
QY 957 MetArgGlnGlyTyrGlnArgGluLeuLeuTyrGlnArgGluAspGlySerPheSerAla 976
DB 3022 CTCACACTGGTTACACAGACAGTGAACACTAACAACACTATGATGCTCTTACACACC 3081
QY 977 PheGly---AsnTyrAspProSer---GlySerThrTrpLeuSerAlaPheValLeuArg 994
DB 3082 TTTCGGGAGCGATATGCGAGCAACAGGCAACACCTGGCTCACAGCCTTTGTCTGAAG 3141
QY 995 CysPheLeuGluAlaAspProTyrIleAspIleAspGlnAsnValLeuHisArgThrTyr 1014
DB 3142 ACTTTTCCCAAGCTCGAGCTACATCTTCATCGATGAAGCACACATTACCCAGGCCCTC 3201
QY 1015 ThrTrpLeuLysGlyHisGlnLysSerAsnGlyGluPheTrpAspProGlyArgValIle 1034
DB 3202 ATATGGCTCTCCAGAGCGAGAGGACAAATGGCTGTTTCAGGAGCTCTGGGTCACTGCTC 3261
QY 1035 HisSerGluLeuGlnGlyLysLysSerProValThrLeuThrAlaTyrIleValThr 1054
DB 3262 AACCAATGCCATAAAGGGAGGAGTAGAAGTGAAGTCAACCTCTCCGCTATATCACCATC 3321
QY 1055 SerLeuLeuGlyTyrArgLysTyrGlnProAsnIleAspValGlnGluSerIleHisPhe 1074
DB 3322 GCCCTTCTGGAGATTCTCTCACAGTCACCTACCTGTTGTCGCAATGCCCTGTTTGC 3381
QY 1075 LeuGluSer-----GluPheSerArgGlyIleSerAspAsnTyrThr 1088
DB 3382 CTGAGTCAGCGCTGGAAGACAGCACAGAAGGGAGCCATGCC---AGCCATGTATATACC 3438
QY 1089 LeuAlaLeuIleThrTyrAlaLeuSerSerValGlySer---ProLysAlaLysGluAla 1107
DB 3439 AAAGCACTGTGGCCTATGCTTTTGGCCTGGCAGGTAAACCCAGGACAGAGGAAGGA 3498
QY 1108 LeuAsnMetLeuThrTrpArgAlaGluGlnGlyGlyMetGlnPheTrp----- 1124
DB 3499 CTCAAGTCACCTAATAGGAAGCTGTGAAGAACAGACACTCTGTCATTGGGAGGCCCT 3558
QY 1125 ValSerSerGluSerLysLeuSerAspSerTrpGlnProArg-----SerLeuAspIle 1142
DB 3559 CAGAAACCCCAAGCAGCCAGTGGGGCAATTTTACGAACCCCGAGCTCCCTCTGCTGAGGTG 3618
QY 1143 GluValAlaAlaTyrAlaLeuSerHisPheLeuGlnPheGln-----ThrSer 1159
DB 3619 GAGATGACATCTATGTGCTCTCGCT---TATCTCAGCGCCCGAGCCCAACCTCG 3675
QY 1160 GluGlyIlePro-----IleMetArgTrpLeuSerArgGlnArgAsnSerLeu 1175
DB 3676 GAGCACCTGACCTCTGCAACCAACATCGTGAAGTGGATCAGAAAGCAGCAGATGCCCGAG 3735
QY 1176 GlyGlyPheAlaSerThrGlnAspThrThrValAlaLeuLysAlaLeuSerGluPheAla 1195
DB 3736 GCGCGTTCCTCCACCCAGGACAGTGGTGGCTCTCCATGCTCTGTCCAAATATGGA 3795
QY 1196 AlaLeuMetAsnThrGluArgThrAsnIleGlnValThrValThrGlyProSerSerPro 1215
DB 3796 GCGCCACATTTACC---AGGACTGGGAGGCTGACAGGTGACTATCCAGTCTTCAGGG 3852
QY 1216 SerProLeuAlaValValGln----- 1222
DB 3853 ACATTTTCCAGCAAAATTCAGATGGGACAAACAATCGCCTGTACTGTGAGCAGGTCTCA 3912
QY 1223 -----ProMetAlaValAsnIleSerAlaAsnGlyPheGlyPheAlaIleCys 1238
DB 3913 TTGCGCAGAGCTGCTGGGGAATACAGCATGAAGTGACAGGAGAGGATGTGCTACCTC 3972
QY 1239 GlnLeuAsnValValTyrAsnValLysAlaSerGlySerSerArgArgArgSerIle 1258

DB 3973 CAGACCTCTCTGAAATACAAATATT-----CTC 3999
QY 1259 GlnSerGlnGluAlaPheAspLeuAspValAlaValLys-----GluAsnLysAsp 1275
DB 4000 CCAGAAAAGGAGAGTTCCTTTGCTTTAGGAGTGAGAGCTCTGCCCTCAACTTGTGAT 4059
QY 1276 AspLeuAsn---HisValAspLeuAsnValCysThrSerPheSerGlyProGly----- 1292
DB 4060 GAACCCAAAGCCACACACAGCTTCCAAATCTCCCTAAGTGTCACTTACACAGGAGCCGC 4119
QY 1293 ---ArgSerGlyMetAlaLeuMetGluValAsnLeuLeuSerGlyPheMetValProSer 1311
DB 4120 TCTGCTCCAAACATGGCGATCGTTGATGTGAAGATGGTCTCTGCTTCATTCCCTCGAAG 4179
QY 1312 GluAlaIleSerLeu-----SerGluThrValLysValGluTyrAspHisGly 1328
DB 4180 CCAACAGTGAATAATGCTTGAAGAATCTTAACCATGTGAGCCGACAGAGTCAGCAGCAAC 4239
QY 1329 LysLeuAsnLeuTyrLeuAspSerValAsnGluThrGlnPheCysValAsnIleProAla 1348
DB 4240 CATGCTTGTGATTACCTTGATAAGGTGTCAAAATCAGACACTGAGCTTGTCTTCACGGTT 4299
QY 1349 ValArgAsnPheLysValSerAsnThrGlnAspAlaSerValSerIleValAspTyrTyr 1368
DB 4300 CTGCAAGATGTCCCGAGTAAGAGATCTCAACCCAGCCATAGTGAAGTCTATGATTACTAC 4359
QY 1369 GluProArgArgGlnAlaValArgSerTyrAsnSer 1380
DB 4360 GAGACGGATGAGTTTGCAATCGCTGAGTACAATGCT 4395

Search completed: August 18, 2004, 08:57:54
Job time : 1752 secs

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OM protein - nucleic search, using frame_plus_p2n model

Run on: August 18, 2004, 00:38:25 ; Search time 214 seconds

(without alignments)

3703.130 Million cell updates/sec

Title: US-10-020-095-4

Perfect score: 7348

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Scoring table: BLOSUM62

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Ygapop 10.0 , Ygapext 0.5

Fgapop 6.0 , Fgapext 7.0

Delop 6.0 , Delext 7.0

Searched: 682709 seqs, 277475446 residues

Total number of hits satisfying chosen parameters: 1365418

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Command line parameters:

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-DB=Issued Patents NA -QFMT=fastap -SUFFIX=p2n.rni -MINMATCH=0.1 -XOOPCL=0
-LOPEXT=0 -UNITS=bits -START=1 -END=1 -MATRIX=blosum62 -TRANS-human4.0.cd
-LIST=45 -DOCALIGN=200 -THR SCORE=spect -THR MAX=100 -THR MIN=0 -ALIGN=15
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-NO MMAP -LARGEQUERY -NEG SCORES=0 -WAIT -DSPBLOCK=100 -LONGLOG
-DEV TIMEOUT=120 -WARN TIMEOUT=30 -THREADS=1 -XGAPOP=10 -XGAPEXT=0.5 -FGAPOP=6
-FGAPEXT=7 -YGAPOP=10 -YGAPEXT=0.5 -DELOP=6 -DELEXT=7

Database : Issued Patents NA.*

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4: /cgn2_6/ptodata/2/ina/6B.COMB.seq.*

5: /cgn2_6/ptodata/2/ina/PCTUS.COMB.seq.*

6: /cgn2_6/ptodata/2/ina/backfiles1.seq.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	4535.5	61.7	3033	US-09-833-381-1810	Sequence 1810, Ap
2	1441	19.6	4577	US-09-241-606-1	Sequence 1, Appl
3	1412	19.2	4792	US-09-566-321-109	Sequence 109, App
4	1346.5	18.3	4079	US-09-016-434-1174	Sequence 1174, Ap
5	973.5	13.2	5211	US-08-447-411-1	Sequence 1, Appl
6	931	12.7	5056	US-08-793-126-2	Sequence 2, Appl
7	931	12.7	5056	US-09-132-271-2	Sequence 2, Appl
8	931	12.7	5067	US-09-142-334-23	Sequence 23, Appl
9	930	12.7	5129	US-09-566-321-107	Sequence 107, App
10	894	12.2	5948	US-08-662-227-1	Sequence 1, Appl
11	894	12.2	5948	US-09-017-947-1	Sequence 1, Appl
12	894	12.2	5948	US-09-925-442-1	Sequence 1, Appl

13	885	12.0	5924	1	US-08-447-411-44	Sequence 44, Appl
14	768.5	10.5	4138	1	US-08-447-411-75	Sequence 75, Appl
15	768.5	10.5	4138	2	US-08-662-227-33	Sequence 33, Appl
16	768.5	10.5	4138	4	US-09-017-947-33	Sequence 33, Appl
17	768.5	10.5	4138	4	US-09-925-442-33	Sequence 33, Appl
18	272.5	3.7	5004	4	US-09-489-039A-4453	Sequence 4453, Ap
19	245	3.3	18431	4	US-09-221-017B-1090	Sequence 1090, Ap
20	234	3.2	339	4	US-09-311-352B-1	Sequence 1, Appl
21	215.5	2.9	750	4	US-09-241-606-3	Sequence 3, Appl
22	211.5	2.9	5151	4	US-09-543-681A-3437	Sequence 3437, Ap
23	203.5	2.8	14066	4	US-09-601-188-36	Sequence 56, Appl
24	185	2.5	549	4	US-09-311-352B-3	Sequence 3, Appl
25	185	2.5	7158	4	US-09-543-681A-2132	Sequence 2132, Ap
26	180	2.4	4026	4	US-09-252-991A-10214	Sequence 10214, A
27	177.5	2.4	8334	4	US-09-543-681A-1952	Sequence 1952, Ap
28	174.5	2.4	7101	1	US-08-480-604A-9	Sequence 9, Appl
29	174.5	2.4	7101	2	US-08-405-496A-9	Sequence 9, Appl
30	174.5	2.4	7101	3	US-08-915-136-9	Sequence 9, Appl
31	174.5	2.4	7101	4	US-08-957-310-9	Sequence 9, Appl
32	174.5	2.4	7101	4	US-10-011-366-9	Sequence 9, Appl
33	174.5	2.4	7101	4	US-09-084-517-9	Sequence 9, Appl
34	171	2.3	9873	4	US-09-328-352-1360	Sequence 1360, Ap
35	165.5	2.3	7577	4	US-09-637-048C-3	Sequence 3, Appl
36	165.5	2.3	7621	4	US-09-637-048C-6	Sequence 6, Appl
37	165	2.2	6114	4	US-09-543-681A-1365	Sequence 1366, Ap
38	165	2.2	28473	4	US-08-961-527-83	Sequence 83, Appl
39	164.5	2.2	4977	4	US-09-071-035-257	Sequence 257, App
40	164.5	2.2	4977	4	US-09-071-035-261	Sequence 261, App
41	164.5	2.2	4977	4	US-09-071-035-265	Sequence 265, App
42	164.5	2.2	13993	4	US-09-220-132-20	Sequence 20, Appl
43	163.5	2.2	13930	4	US-09-976-594-1011	Sequence 1011, Ap
44	163.5	2.2	14070	4	US-09-108-006C-2	Sequence 2, Appl
45	163	2.2	37948	3	US-09-251-645-11	Sequence 11, Appl

ALIGNMENTS

RESULT 1
US-09-833-381-1810
; Sequence 1810, Application US/09833381
; Patent No. 6672186
; GENERAL INFORMATION:
; APPLICANT: Robison, Keith E.
; TITLE OF INVENTION: No. 6672186el Nucleic Acid and Protein Homologs
; FILE REFERENCE: 5800-119
; CURRENT APPLICATION NUMBER: US/09/833,381
; CURRENT FILING DATE: 2001-04-11
; PRIOR APPLICATION NUMBER: 09/516,448
; PRIOR FILING DATE: 2000-02-29
; NUMBER OF SEQ ID NOS: 2050
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 1810
; LENGTH: 3033
; TYPE: DNA
; ORGANISM: Homo sapiens
US-09-833-381-1810

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Score: 4535.50
Percent Similarity: 98.00%
Best Local Similarity: 97.78%
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Length: 3033
Matches: 880
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Mismatches: 1
Indels: 17
Gaps: 1

US-10-020-095-4 (1-1428) x US-09-833-381-1810 (1-3033)

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QY 1389 LeuCysSerAspValGlnGlyCysArgProCysGluAspGlyAlaSerGlySerHisHis 1408
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QY 1409 HisSerValIlePheIlePheCysPheLysLeuLeuTyrPheMetGluLeuTyrLeu 1428
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RESULT 2

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US-09-241-606-1
; Sequence 1, Application US/09241606
; Patent No. 6472140
; GENERAL INFORMATION:
; APPLICANT: Tanzi, Rudolph E.
; APPLICANT: Kovacs, Dora
; APPLICANT: Saunders, Aleister J.
; TITLE OF INVENTION: Alpha-2-Macroglobulin Therapies and Drug Screening Methods for
; FILE OF INVENTION: Alzheimer's Disease
; FILE REFERENCE: 0609.4450003
; CURRENT APPLICATION NUMBER: US/09/241,606
; CURRENT FILING DATE: 1999-02-02
; NUMBER OF SEQ ID NOS: 27
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 1
; LENGTH: 4577
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: sig_peptide
; LOCATION: (44)..(112)
; FEATURE:
; NAME/KEY: CDS
; LOCATION: (44)..(4468)
; FEATURE:
; NAME/KEY: mat_peptide
; LOCATION: (113)..(4468)
US-09-241-606-1

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Query Match: 19.61% Indels: 284
DB: 4 Gaps: 59

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US-10-020-095-4 (1-1428) x US-09-241-606-1 (1-4577)

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QY 32 AlaProGlyIleIleArgProGlyGlyAsnValThrIleGlyValGluLeuLeuGluHis 51

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Db 203 CTGAATGAGACAGTGAAGTCTTCTTGGAGTCTGTACGGGGAACAGGAGCTC 262
QY 72 ---SerValLeuGluAlaGluGly---ValPheGluLysGlySerPheLysThrLeuThr 89
Db 263 TTCCTGCTGAGCGGAGGAATGACGTACTCCACTGTGCTGCTTC- 310
QY 90 LeuProSerLeuProLeuAsnSerAlaAspGlu-----IleTyrGluLeuArgVal 106
Db 311 -----GCTGCCAAAGCTCTTCATCAATGAGAGGTAATGTTCTCCTCACTGTCAGTG 364
QY 107 ThrGlyArgThrGlnAspGluIleLeuPheSerAsnSerThrArgLeuSerPheGluThr 126
Db 365 AAAGGACCAACCCAAAGAA-----TTTAAAGACGGACCAACAGTGATGGTTAAGAAC 415
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QY 167 Leu-----IleLysAspProLysSerAsnLeuIleGlnGlnThrLeuSerGlnSerAsp 185
Db 536 GTATACATTCAGGATCCCAAGAAATCGCATCGCAATGCGAGAGTTCCAGTTAGAG 595
QY 186 LeuGlyValIleSerLysThrPheGlnLeuSerSerHisProIleLeuGlyAspTyrSer 205
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QY 206 IleGlnValGlnValAsnAsp-----GlnThrTyrTyrGlnSerPheGlnValSerGlu 223
Db 656 GTGTGTTGTACAGAAATAATCAGTGGAAAGGACAGAGCAC---CCTTCCAGCTGAGGAA 712
QY 224 TyrValLeuProLysPheGluValThrLeuGlnThrProLeuTyrCysSerMetAsnSer 243
Db 713 TTTGTTCTTCCCAAGTTTGAAGTACAGTACAGTGCACAAAGATAATCACCATTGGA 772
QY 244 LysHisLeuAsnGlyThrIleThrAlaLysTyrThrTyrGlyLysProValLysGlyAsp 263
Db 773 GAAGAGATGATGATCAGTGTGTGGCTATACACATATGGAAGCCTGTCCCTGGACAT 832
QY 264 ValThrLeuThrPheLeuProLeu----- 271
Db 833 GTGACTGTGAGCATTTGCAAGAAAGTATAGTGACGCTCCGACTGCCACGTGAAGATTCA 892
QY 272 -----SerPheTyrGlyLys 276
Db 893 CAGGCTTCTGTGAGAAATTCAGTGGACAGCTAAACAGCCATGGCTGTCTTATCAGCAA 952
QY 277 LysLysAsnIleThrLysThrPheLysIleAsnGlySerAlaAsnPheSerPheAsnAsp 296
Db 953 GTAAAA-----ACCAAGGTCTTCCAGCTGAAGAG-----AAGGAG 988
QY 297 GluGluMetLysAsnValMetAspSerSerAsnGlyLeuSerGluTyrLeuAspLeuSer 316
Db 989 TATGAATGAAGAA-----CTTCACACTGAGGCCAGATCCAA 1024
QY 317 SerProGlyProValGluIleLeuThr-----ThrValThrGluSerVal 331
Db 1025 GAAGAAGGAACAGTGTGTGAATTTGACTGGAAGGAGTCCAGTGAATAATCACAAGAACCATA 1084
QY 332 ThrGlyIleSerArgAsnValSerThrAsnValPhePheLysGlnHisAspTyrIleIle 351
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QY 352 GluPhePheAspTyrThrThrValLeuLysProSerLeuAsnPheThrAlaThrValLys 371

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[illegible]

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Db      4283  CATGCTCTGATTACCTTTGATAAGGTGTCAAATCAGACACTGAGCTTGTTCTTCAAGGTT 4342
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RESULT 3
US-09-566-921-109
; Sequence 109, Application US/09566921
; Patent No. 6682888
; GENERAL INFORMATION:
; APPLICANT: Loring, Jeanne F.
; APPLICANT: Tingley, Debora W.
; APPLICANT: Edwards, Carla M.
; TITLE OF INVENTION: GENES EXPRESSED IN ALZHEIMER'S DISEASE
; FILE REFERENCE: PA-0024 US
; CURRENT APPLICATION NUMBER: US/09/566,921
; CURRENT FILING DATE: 2000-05-05
; NUMBER OF SEQ ID NOS: 138
; SOFTWARE: PERL Program
; SEQ ID NO 109
; LENGTH: 4792
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: misc feature
; OTHER INFORMATION: incyte ID No. 6682888 369213.15
US-09-566-921-109

Alignment Scores:
Pred. No.: 7e-142 Length: 4792
Score: 1412.00 Matches: 451
Percent Similarity: 46.14% Conservative: 266
Best Local Similarity: 29.02% Mismatches: 551
Query Match: 19.22% Indels: 286
DB: 4 Gaps: 59

US-10-020-095-4 (1-1428) x US-09-566-921-109 (1-4792)

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Qy      32  AlaProGlyIleIleArgProGlyGlyAsnValThrIleGlyValGluLeuGluHis 51
Db      341  GTCCCTCTCCCTGCCACT--GAGACCAGTGAAGAGGCTGTGCTCTTGAGCTAC 397
Qy      52  CysProSerGlnValThrValLysAlaGluLeuLeuLysThrAlaSerAsnLeuThrVal 71
Db      398  CTGAATGAGACAGTGAAGTGTAAAGTGTCTCTGGAGTCTGTGAGGGGAAACAGGAGCCTC 457
Qy      72  --SerValLeuGluAlaGluGly--ValPheGluLysGlySerPheLysThrLeuThr 89
Db      458  TTCACTCACTGGAGGGGGAGATGACTACTCCACTGTGCGCTTC----- 505
Qy      90  LeuProSerLeuProLeuAsnSerAlaAspGlu-----IleTyrGluLeuArgVal 106
Db      506  -----GCTGTCCCAAAGTCTTCATCCAAATGAGGAGTAATATGTTTCCTCACTGTCCAAGT 559
Qy      107  ThrGlyArgThrGlnAspGluIleLeuPhePheSerAsnSerThrArgLeuSerPheGluThr 126
Db      560  AAGGACCAACCCCAAGAA-----TTTAAAGACGGGACCAAGTGTGCTTAAAGAAC 610
Qy      127  LysArgIleSerValPheIleGlnThrAspLysAlaLeuTyrIleProLysGlnGluVal 146

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APPLICANT: Janice Au-Young
 APPLICANT: Jeffrey J. Seilhamer
 TITLE OF INVENTION: COMPOSITION FOR THE DETECTION OF SIGNALING
 TITLE OF INVENTION: PATHWAY GENE EXPRESSION

NUMBER OF SEQUENCES: 1490
 CORRESPONDENCE ADDRESS:
 ADDRESSEE: INCYTE PHARMACEUTICALS, INC.
 STREET: 3174 PORTER DRIVE
 CITY: PALO ALTO
 STATE: CALIFORNIA
 COUNTRY: USA
 ZIP: 94304

COMPUTER READABLE FORM:
 MEDIUM TYPE: Floppy disk
 COMPUTER: IBM PC compatible
 OPERATING SYSTEM: PC-DOS/MS-DOS

SOFTWARE: Word Perfect 6.1 for Windows/MS-DOS 6.2
 CURRENT APPLICATION DATA: US/09/016,434

FILING DATE: HEREWITH

CLASSIFICATION:

PRIOR APPLICATION DATA:

APPLICATION NUMBER:

FILING DATE:

CLASSIFICATION:

ATTORNEY/AGENT INFORMATION:

NAME: Zeller, Karen J.

REGISTRATION NUMBER: 37,071

REFERENCE/DOCKET NUMBER: PA-0002 US

TELECOMMUNICATION INFORMATION:

TELEPHONE: (650) 855-0555

TELEFAX: (650) 845-4166

INFORMATION FOR SEQ ID NO: 1174:

SEQUENCE CHARACTERISTICS:

LENGTH: 4079 base pairs

TYPE: nucleic acid

STRANDEDNESS: single

TOPOLOGY: linear

IMMEDIATE SOURCE:

LIBRARY: GENBANK

CLONE: g177869

US-09-016-434-1174

Alignment Scores:
 Pred. No.: 6,71e-135 Length: 4079
 Score: 1346.50 Matches: 419
 Percent Similarity: 46.66% Conservative: 238
 Best Local Similarity: 29.76% Mismatches: 488
 Query Match: 18.32% Indels: 263
 DB: 4 Gaps: 54

US-10-020-095-4 (1-1428) x US-09-016-434-1174 (1-4079)

Qy 12 LeuLeuCysValCysThrAlaAlaLeuAlaValAlaProGlyProArgPheLeuValThr 31
 Db 86 CTCTGGTCTCTCCGCCACAGAGCGCTCAGTCTCTGGAACCCGAGTATATGTTCTG 145
 Qy 32 AlaProGlyIleAlaArgProGlyGlyAsnValThrIleGlyValGluLeuGluHis 51
 Db 146 GTCCCTCCCTGCTCCACACT---GAGACACTGAGAGGGCTGTCTCTCTGAGCTAC 202
 Qy 52 CysProSerGlnValThrValValValAlaGluLeuLysThrAlaSerAsnLeuThrVal 71
 Db 203 CTGAATCAGACAGTGTAGTGTCTCTCTGAGTCTCTGAGGGAACAGGAGCTC 262
 Qy 72 ---SerValLeuGluAlaGluGly---ValPheGluLysSerPheLeuThr 89
 Db 263 TTCCTGACCTGGAGGGGAGATGAGTACTCCACTGTGTCTGCTC-----310
 Qy 90 LeuProSerLeuProLeuAsnSerAlaAspGlu-----IleYrGluLeuArgVal 106
 Db 311 -----GCTGTCCCAAGTCTTCATCCATGAGGAGTATGTTCTCTCACTGTCCCAAGTG 364

Qy 107 ThrGlyArgThrGlnAspGluIleLeuPheSerAsnSerThrArgLeuSerPheGluThr 126
 Db 365 AAAGGACCAACCCCAAGAA-----TTTAAGAAGCGGACACAGTATGGTTAAGAAC 415
 Qy 127 LysArgIleSerValPheIleGlnThrAspLysAlaLeuTyrLysProLysGlnGluVal 146
 Db 416 GAGGACAGTCTGGTCTTTTCCAGACAGACAAATCAATCATCAACACCGGCGGACAGTG 475
 Qy 147 LysPheArgIleValThrLeuPheSerAspPheLysProTyrLysThrSerLeuAsnIle 166
 Db 476 AAATTCGTGTGTCTCCATGGATGAAACTTTTCCACCCCTCAATGATGATTTCACTCA 535
 Qy 167 Leu---IleLysAspProLysSerAsnLeuIleGlnThrLeuSerGlnSerAsp 185
 Db 536 GTATACATTCAAGATCCCAAGGAAATCGCATGCAATGGCAGAGTTTCCAGTTAGAG 595
 Qy 186 LeuGlyValIleSerLysThrPheGlnSerSerHisProIleLeuGlyAspTrpSer 205
 Db 596 GGTGGCTCAAGCAATTTCTTTTCCCTCTCATCAGAGCCCTTCCAGGGCTCTCTACAAG 655
 Qy 206 IleGlnValGlnValAsnAsp-----GlnThrTyrTyrGlnSerPheGlnValSerGlu 223
 Db 656 GTGGTGTACAGAAAGAAATCAGGTGGAAGGACAGAGCAC---CCTTTCACTGGAGGAA 712
 Qy 224 TyrValLeuProLysPheGluValThrLeuGlnThrProLeuTyrCysSerMetAsnSer 243
 Db 713 TTTGTTCTTCCCAAGTTTGAAGTACAGTACAGTGCCTCAAGATATATCACTCTTGAA 772
 Qy 244 LysHisLeuAsnGlyThrIleThrAlaLysTyrThrTyrGlyLysProValLysGlyAsp 263
 Db 773 GAAGAGATGAATGATCAGTGTGTGGCTATACACATATGGAAGCTGTCTCTCGACAT 832
 Qy 264 ValThrLeuThrPheLeuProLeu-----271
 Db 833 GTGACTGTGAGCATTTGCGAAGATATAGTACGCTCCGACTCCGACGCGTGAAGATCA 892
 Qy 272 -----SerPheTrpGlyLys 276
 Db 893 CAGGCTTCTGTGAGAAATTCAGTGGACAGCTAAACAGCCATGGCTCTCTATCAGCAA 952
 Qy 277 LysLysAsnIleThrLysThrPheLysIleAsnGlySerAlaAsnPheSerPheAsnAsp 296
 Db 953 GTAAAA-----ACCAAGGTCTTCCAGCTGAAGAGG-----AAGGAG 988
 Qy 297 GluGluMetLysAsnValMetAspSerSerAsnGlyLeuSerGluTyrLeuAspLeuSer 316
 Db 989 TATGAATGAAA-----CTTCACACTGAGGCGCCAGATCCAA 1024
 Qy 317 SerProGlyProValGluIleLeuThr-----ThrValThrGluSerVal 331
 Db 1025 GAAGAAGGAACAGTGTGGAATTCAGTGGAGGCGAGTCCAGTGAATCAACAGAACATA 1084
 Qy 332 ThrGlyIleSerArgAsnValSerThrAsnValPhePheLysGlnHisAspTyrIleIle 351
 Db 1085 ACCAACTCTCA---TTTGGAAGTGGACTCAGCTCTTCGACAGGGA-----ATT 1132
 Qy 352 GluPhePheAspTyrThrValLeuLysProSerLeuAsnPheThrAlaThrValLys 371
 Db 1133 CCTTCTTTGGG-----CAG 1147
 Qy 372 ValThrArgAlaAspGlyAsnGlnLeuThrIleGluArgAsnAsnValIle 391
 Db 1148 GTGGCCCTAGTAGATGGAAAGGCGTCCCTATACCA-----ATAAAGTCTATA 1195
 Qy 392 ThrValThrGlnArgAsnTyrThrGluTyrTrpSerGlySerAsnSerGlyAsnGlnLys 411
 Db 1196 TTCATC---AGAGGAATGAACAACTATTAC-----TCCAATGCTACCCGAGTAG 1246
 Qy 412 MetGluAlaValGln---LysIleAsnTyrThr-----ValProGlnSerGlyThrPhe 428
 Db 1247 CATGGCTTGTACAGTCTCTTATCAACACCACCAACCGTATGGGTACTCTCTTACTGTT 1306
 Qy 429 LysIleGluPhePro-----IleLeuGluAspSer 438

Db	1307	AGGGTCAATTACAAGATCGTAGTCCCTGTTACGGCTACCAAGTGGGTGTCAGAAGACAC	1366
Qy	439	SerGluLeuGlnLeuLeuLeuAlaTyrPheLeuGlySerLysSerMetAlaValHisSer	458
Db	1357	GAAGAGGCACATCACATGCTTAT	1390
Qy	459	LeuPheLysSerProSerLysThrTyrIleGlnLeuLysThrArgAspGluAsnIleLys	478
Db	1391	CTTGTGTTCTCCCAAGCAAGAGCTTTGTCACCTTGAGCCCATGTCTCATGAACATCCC	1450
Qy	479	ValGlySer-----ProPheGluLeuValSerGlyAsnLys-----Arg	492
Db	1451	TGTGCCCATCTACAGACAGTCCAGGCACATTATTTCTGAATGAGGACCCCTGCTGGG	1510
Qy	493	LeuLysGluLeuSer-----TyrMetValValSerArgGlyGlnLeuValAlaValGly	510
Db	1511	CTGAGAAGAGCTCTCTTTTATATCTGATAATGCAAGGAGGAGCAATTGTCGAACATGGG	1570
Qy	511	-----LysGlnAsnSerThr-----MetPheSerLeuThr	520
Db	1571	ACTCATGGACTCTGTGTAAGCAGGAAGACATGAAGGCCATTTTTCCATCTCAATCCCT	1630
Qy	521	ProGluAsnSerTrpTrpProLysAlaCysValIleValTyrTyrIleGluAspAspGly	540
Db	1631	GTGAAGTCAGACATGTCTCTGTCGCTCGGTGTCTCATCTATGCTGTTTACCTACCGGG	1690
Qy	541	GluIleLeuSerAspValLeuLysIleProValGlnLeuValPheLysAsnLysIleLys	560
Db	1691	GACGTGATTGGGATTCGCAAAATATGATGTTGAAAATTGTCGGCCCAACAGGTGGAT	1750
Qy	561	LeuTyrTrpSerLysValLysAlaGluProSerGluLysValSerLeuArgIleSerVal	580
Db	1751	TTGAGCTTCAGCCCATCACAAGTCTCCAGCCTCACAGCCACCTGCAGTCACAGCG	1810
Qy	581	ThrGlnProAspSerIleValGlyIleValAlaValAspLysSerValAsnLeuMetAsn	600
Db	1811	GCT---CCTCAGTCCGTGCGCCCTCCGTGCTGTGACCAAGCGTGTGCTCACTGAAG	1867
Qy	601	AlaSerAsnAspIleThrMetGluAsnValValHisGluLeu---GluLeuTyrAsnThr	619
Db	1868	CCTGATGCTGAGCTCTCGGCGTCTCGTGTACACCTGTACCAGAAAGGACCTCACT	1927
Qy	620	GlyTyr-----TyrLeuGlyMet	625
Db	1928	GGCTTCCCTGGCGCTTTGAATGACACGAGCATGAAGACTGCATCAATGCTCATATGTC	1987
Qy	626	PheMetAsnSer-----PheAla	631
Db	1988	TATATTATGGAATCACATATATCTCCAGTATCAAGTACAAATGAAAGGATATGTACAGC	2047
Qy	632	ValPheGlnGluCysGlyLeuTrpValLeuThrAspAlaAsnLeuThrLysAspTyrIle	651
Db	2048	TTCTAGAGACATGGCTTAAAGGCATTACCAACTCAAAGATTCTGTAACCCCAAAATG	2107
Qy	652	AspGlyValTyrAspAsnAlaGlu-----Tyr	660
Db	2108	TGTCACAGCTTCACAGTATGAATGCATGGACCTGAAGTCTACGTAGGTTTTTAT	2167
Qy	661	AlaGluArgPheMetGluGluAsnGluGlyHisIleValAspIleHisAspPheSerLeu	680
Db	2168	GAGTCAGATGATATGGAAGAGGCCATGTCAGCGCTGTGTGATGTTCAAGAG-----	2218
Qy	681	GlySerSerProHis-----ValArgLysHisPheProGluThrTrpIleTrpLeu	697
Db	2219	-----CCTCACAGGAGACCGTACGAAAGTACTTCCCTGAGACATGGATCTGGGAT	2269
Qy	698	AspThrAsnMetGlyTyrArgIleTyrGlnGluPheGluValThrValProAspSerIle	717
Db	2270	TTGTGTGTGTTAAACTCAGCAGGGGTGGCTGAGTAGGAGTAACAGTCCCTGCACCATC	2329
Qy	718	ThrSerTrpValAlaThrGlyPheValIleSerGluAspLeuGlyLeuGlyLeuThrThr	737

2330	Db	ACCGATGGAAAGCAGGGGCTTCTGCTCTCTGAAGATGCTGCAGATTGGTATCTCTTCC	2389
738	Qy	ThrProValGluLeuGlnAlaPheGlnProPhePheIlePheLeuAsnLeuProTyrSer	757
2390	Db	ACT---GCCCTCTCCGAGCCTCCAGCCCTCTTTTGGAGCTTCAATGCGCTTACTCT	2446
758	Qy	ValIleArgGlyGluGluPheAlaLeuGluIleThrIlePheAsnTyrLeuIlysAspAla	777
2447	Db	GTGATTGGTGAGAGGCGCTTCACACTCAAGGCCACGGCTCTAAACTACCTTCCCAATGC	2506
778	Qy	ThrGluValIysValIleIleGluIySerAspIysPheAspIleLeuMetThrSerSer	797
2507	Db	ATCCGGGTCAGTGTGCAGCTGGAAAGCCTCTCCGCCCTTCTTCTGCTGCCAGTGGAGAAG	2566
798	Qy	Glu-----IleAsnAlaThrGlyHisGlnGlnThrLeuLeuValProSer	812
2587	Db	GAACAAGCGCGCTCACTGCATCTGTGCAACGGCGGCA	2605
813	Qy	GluAspGlyAlaThrValLeuPheProIleArgProThrHisLeuGlyGluIleProIle	832
2606	Db	-----ACTGTCTCTGGCGATTAACCCCAAGTCATTAGGAATGGAATTC	2653
833	Qy	ThrValThrAlaLeuSer-----	841
2654	Db	ACTGTAGCGCAGAGCACTAGAGTCTCAAGAGCTGTGTGGAGCTCAGGTGCCTTCAGTT	2713
842	Qy	-----SerAspAlaValThrGlnMetIleLeuValIysAlaGluGlyIle	856
2714	Db	CCTGAACACGGAAGAAAGACACAGTCATCAAGCCCTCTGTGTGTTGAACTGAAGACTA	2773
857	Qy	GluIysSerTyrSerGlnSerIleLeuLeuAspLeuThrAspAsnArgLeuGlnSerThr	876
2774	Db	GAGAAGAAACAACATTCAACTCCCTACTTTGTCCATCAGGTGGTGAGTTCT-----	2827
877	Qy	LeuIysThrLeuSerPheSerPheProProAsnThrValThrGlySerGluArgValGln	896
2828	Db	--GAAGAAATTATCCCTGAAACTGCCACCAATATGTGTAGAGAATCTCCGAGGCTCT	2884
897	Qy	IleThrAlaIleGlyAspValLeuGlyProSerIleAsnGlyLeuAlaSerLeuIleArg	916
2885	Db	GTCTCAGTTTGGGAGACATATTAGCTCTGCCATGCCAAAACACAAAATCTTCTCCAG	2944
917	Qy	MetProTyrGlyCysGlyGluGlnAsnMetIleAsnPheAlaProAsnIleTyrIleLeu	936
2945	Db	ATGCCCTATGGCTGTGGAGAGCAATATGGTCTCTTTGTCTTAACATCTATGTACTG	3004
937	Qy	AspTyrLeuThrIyIysIyIysGlnLeuThrAspAsnLeuIyIysGluIyIysAlaLeuSerPhe	956
3005	Db	GAITATCTAATGAACACAGCAGCTTATCTCCAGAGTCAAGTCCAGGCCCATGGCTAT	3064
957	Qy	MetArgGlnGlyTyrGlnArgGluLeuLeuTyrGlnArgIleuAspGlySerPheSerAla	976
3065	Db	CTCAACACTGTTTACCAGAGACAGATTGAACTACAAACACTATGATGGCTCTTACAGCAC	3124
977	Qy	PheGly---AsnTyrAspProSer---GlySerThrTyrIleuSerAlaPheValLeuArg	994
3125	Db	TTTGGGAGCGATATGCGAGAACCGAGGCAACACTGGCTCACAGCCCTTGTCTCTGAAG	3184
995	Qy	CysPheLeuGluAlaAspProTyrIleAspIleAspGlnAsnValLeuHisArgThrTyr	1014
3185	Db	ACTTTTGGCCAGCTCGAGCTTACATCTTCATCGATGAGCACACATATCCCAAGCCCTC	3244
1015	Qy	ThrTyrIleuIysGlyHisGlnIySerAsnGlyGluPheTyrAspProGlyArgValIle	1034
3245	Db	ATATGCTCTCCAGAGGAGGAGGACATGGCTGTTTCAGAGCTCTGGGTCACTGTCTC	3304
1035	Qy	HisSerGluLeuGlnGlyIyAsnIySerProValThrLeuThrAlaTyrIleValThr	1054
3305	Db	AACAATGCCATAAAGGAGAGTAGAAGTAGAGTGAGCTCTCCGCTTATATCAATC	3364
1055	Qy	SerLeuLeuGlyTyrArgIyIysTyrGlnProAsnIleAspValGlnIySerIleHisPhe	1074
3365	Db	GCCTTCTGGAATTCCTCTCACGTCACTACCTCGTGTTCGCAATGCGCTGTTTGC	3424

528 AGTTCTAAACAGTCAATCCATCAGCTCGATCCGGCCCTTACAATTTACAGAGCTTGC 587
 201 ---LeuGlyAspTrpSerIleGlnValGlnValAsn-----AspGlnThrTyrTyr 216
 588 AGTTTGGGACATGGAAGCTGGCCAAATATGACATTCACCAGAGAGCTACACT 647
 217 GlnSerPheGlnValSerGluTyrValLeuProLysPheGluValThrLeuGlnThrPro 236
 648 GCATATTTTGAATCAGAGATATGTTTACCAAGCTTTGAAGTCGCTGCAACCATCA 707
 237 -----LeuTyrCysSerMetAsnSerLysHisLeuAsnGlyThrIleThrAlaLys 253
 708 GATAAGTTCTTTACATGATGGGAAT---AAAATTTCCAGTGTCTATCTATCGAAG 764
 254 TyrThrTyrGlyLysProValLysGlyAspValThrLeuThrPheLeuProLeuSerPhe 273
 765 TACTTATATGGAAGAAAGTGAAGCT---GTGGCCCTTTGTCTCTTTGGAGTCAAAATA 821
 274 TrpGlyLysLysLysAsnIle-----ThrLysThrPheLysIleAsnGlySer 289
 822 GATGATGCTAAAGAGATATTCAGACTCACTCAGAGAAATCCGATTAATTATGAGAGAT 881
 290 AlaAsnPheSerPheAsnAspGluMetLysAsnValMetAspSerSerAsnGlyLeu 309
 882 GGGGAAGCAACACTAAAGAGATACACTACGTTCCCGATTTCAAGATCTCAATCAGCTT 941
 310 SerGluTyrLeuAspLeuSerProGlyProValGluLeuThrValThrValThrGlu 329
 942 GTTGGTCATCTCTGTATGTATCT-----GTACAGTGTATACAGAA 983
 330 SerValThrGlyIleSerArgAsnValSerThrAsnValPhePheLysGlnHisAspTyr 349
 984 TCAGGAGTGTATGATGCTAGCTAGCAAGCGGCATTTCATATTGTGACATCTCCCTAT 1043
 350 IleIleGluPhePheAspTyrThrThrValLeuLysProSerLysAsnPheThrAlaThr 369
 1044 CAGATCTACTTCCAAAAAACCCTCAATATTTCAAGCCAGGAATGCCATATGAATCGACG 1103
 370 ValLysValThrArgAlaAspGlyAsnGlnLeuThrLeuGluGluArgAsnVal 389
 1104 GTGTATGTTACCAACCTGATGCTCACCAGCTGCC-----CAT 1142
 390 ValIleThrValThrGlnArgAsnTyrThrGluTyrTrpSerGlySerAsnSerGlyAsn 409
 1143 GTGCCAGTGTATCAGAGGCCATTTCATCTGAG-----GGAACC 1181
 410 GlnLysMetGluAlaValGlnLysIleAsnTyrThrValPro-----GlnSerGly 426
 1182 ACTTTGAGTGTGGGACTGCTAAGCTCATCTGAACACACCACTGAACATTCANAAGC--- 1238
 427 ThrPheLysIleGluPheProIleLeuGluAspSerSerGluLeuGlnLeuLysAlaTyr 446
 1239 -----CTACCGATCACTGTAGNACTAACATGAGGACCTCCAGAGAA 1283
 447 PheLeuGlySerLysSerMetAlaValHisSerLeuPheLysSerProSerLysThr 466
 1284 CGCCAGGCAATAAAGTCCATGACAGCCACAGCCCTACCAAAACCAGGCGGCTCGAAAAC 1343
 467 TyrIleGlnLeuLysThrArgAspGluAsnIleLysValGlySer-----ProPheGlu 484
 1344 TATCTTTCATGACCATTCATCTCAGAGATTAAGCCCGGAGATAACTTACTGTCAAT 1403
 485 LeuValValSerGlyAsn-----LysArgLeuLysGluLeuSerTyrMetVal 500
 1404 TTCAATGTGAGGGCAATGCMAATTTCATGAACCATCATCAATATTTACATACCTCAT 1463
 501 ValSerArgGlyGlnLeuValAlaValGlyLys-----GlnAsnSer 514
 1464 TTGAATAAAGGGAAGATTTTCAAGTTGGCAGCAACCCAGGAGAGATCGGCAGATCTCG 1523
 515 ThrMetPheSerLeuThrProGluAsnSerTrpThrProLysAlaCysValIleValTyr 534

1524 GTGACCATGAATCTGCATATCACTCCAGATCTCATCCCTTCCGTTTGTGGCTTAC 1583
 535 TyrIleGluAspAspGlyGluIleIleSerAspValLeuLysIleProValGln----- 552
 1584 TACCAAGTGGGAATAACGAATTTGTGCTGATTCTGTCTGGTGGTATGTGAAGATACC 1643
 553 -----LeuValPheLys-----AsnLysIleLysLeuTyr 562
 1644 TGCATGGGAAGCTTGGTTGTGAAGAGGAGCGCTTCCAGACAGCATGCAATACAA--- 1697
 563 TrpSerLysValLysAlaGluProSerGluLysValSerLeuArgIleSerValThrGln 582
 1698 -----AAGCCAGAGCTGCAATGAATAAATCAAAATTGGAA---GGGGAT 1736
 583 ProAspSerIleValGlyIleValAlaValAspLysSerValAsnLeuMetAsnAlaSer 602
 1737 CCAGTGTCTCGGTTGTCTTGTGGCTGTGGACAACAGCATATATGTCTCAATGATAAA 1796
 603 AsnAspIleThrMetGluAsnValHisGluLeuLeuTyrAsnThrGlyTyrTyr 622
 1797 TATAAGATTAGCAAGCTAAGATATGGGACACATAGAAAAGATGACTTTGGTGTGACA 1856
 623 LeuGlyMetPheMetAsnSerPheAlaValPheGlnGlyCysGlyLeuTrpValLeuThr 642
 1857 GCTGGCAGTGGCCAGATAATCTGGGTGTGTTTGAAGATGCTGAGCTGGCTCTGACAAC 1916
 643 AspAlaAsnLeuThr----- 647
 1917 AGCTAATCTCAACACCAACACAGAGATCAGCTCAAGTGTCTCAGCTTGCAAAATCGG 1976
 647 ----- 647
 1977 AGCGTGCAGCTTCTGTTTTGCTGTGACAGCAAGCAAGCAAGCGGACAGCTTTCAG 2036
 648 -----LysAspTyrIleAspGlyValTyrAspAsn----- 657
 2037 GATCAAGCCCTCGCTAAATGCTGTGAAGATGGCATGATGAGAACCCCATGGGTACACT 2096
 658 AlaGluTyrAlaGluArgPheMetGluGluAsnGluGly----- 670
 2097 TGTGNAAGCGTGCAAAATACATCCAGGAGGAGATGCTTGTAAAGCTGCCTTCTTGA 2156
 671 -----HisIleVal----- 673
 2157 TGTGTCTACTACATCAAGGGATCCGAGATGAAACCAACCGGAGAGCGAGTGTCTTCTG 2216
 674 -----AspIleHisAspPheSerLeuGlySerProHisVal---ArgLysHis 689
 2217 GCAAGAGTGAATTTTGAAGATGAACCTCTTGGAGATGACACATCATCTCCAGTCTGAT 2276
 690 PheProGluThrTrpIleTrpLeu-----AspThrAsnMetGly 702
 2277 TTTCCGAGAGTGTGTTGTGGCTAACAGAGGAATTGACCGGGAGCCTAACATCAAGGG 2336
 703 TyrArgIleTyrGlnGluPheGluValThrValPro-----AspSerIleThr 718
 2337 ATTTCA-----AGCAAGACAGTACCTTTTATCTGAGGGATTCATCACA 2381
 719 SerTrpValAlaThrGlyPheValIleSerGluAspLeuGlyLeuGlyLeuThrThr 738
 2382 ACTTGG-----CAGTGTGCTGGTGGGCTTTTCCACCAC 2417
 739 -----ProValGluLeuGlnAlaPheGlnProPhePheIlePhe 751
 2418 AAAGGATCTGTGTGGCTGGAACCGTATGAATAACAGTCATGAAGAGCTTCTTCATTGAT 2477
 752 LeuAsnLeuProTyrSerValIleArgGlyGluGluPheAlaLeuGluIleThrIlePhe 771
 2478 CTTGACTGCCATATTCAGTAGTAAGANTGAGGAGTGGAGATTCGAGCTATTCTGTAC 2537
 772 AsnTyrLeuLysAspAlaThrGluValLysValIleIleGluLysSerAspLysPheAsp 791
 2538 AACTACGCTGACGAGGATATTTATGTGGAGTGGAACTGATATACACCCAGCCCTTC--- 2594

US-08-793-126-2
 ; Sequence 2, Application US/08793126
 ; Patent No. 5849297
 ; GENERAL INFORMATION:
 ; APPLICANT: Harrison, Richard Alexander
 ; APPLICANT: Farris, Charles Timothy
 ; TITLE OF INVENTION: MODIFIED HUMAN C3 PROTEINS
 ; NUMBER OF SEQUENCES: 2
 ; CORRESPONDENCE ADDRESS:
 ; ADDRESSEE: HALE AND DORR LLP
 ; STREET: 60 State Street
 ; CITY: Boston
 ; STATE: MA
 ; COUNTRY: United States of America
 ; ZIP: 02109
 ; COMPUTER READABLE FORM:
 ; MEDIUM TYPE: Floppy disk
 ; COMPUTER: IBM PC compatible
 ; OPERATING SYSTEM: PC-DOS/MS-DOS
 ; SOFTWARE: PatentIn Release #1.0, Version #1.30
 ; CURRENT APPLICATION DATA:
 ; APPLICATION NUMBER: US/08/793,126
 ; FILING DATE: 07-FEB-1997
 ; CLASSIFICATION: 424
 ; ATTORNEY/AGENT INFORMATION:
 ; NAME: Baker, Hollie L.
 ; REGISTRATION NUMBER: 31,321
 ; REFERENCE/DOCKET NUMBER: 102286.377
 ; TELECOMMUNICATION INFORMATION:
 ; TELEPHONE: (617) 526-6000
 ; TELEFAX: (617) 526-5000
 ; INFORMATION FOR SEQ ID NO: 2:
 ; SEQUENCE CHARACTERISTICS:
 ; LENGTH: 5056 base pairs
 ; TYPE: nucleic acid
 ; STRANDEDNESS: single
 ; TOPOLOGY: linear
 ; MOLECULE TYPE: cDNA
 ; US-08-793-126-2

Alignment Scores:
 Pred. No.: 1,2e-89 Length: 5056
 Score: 931.00 Matches: 381
 Percent Similarity: 40.88% Conservative: 287
 Best Local Similarity: 23.32% Mismatches: 609
 Query Match: 12.67% Indels: 358
 DB: 2 Gaps: 63

US-10-020-095-4 (1-1428) x US-08-793-126-2 (1-5056)

Qy 3 GlyProLeuThrAlaAlaHisLeuLeuCysValCysThrAlaAlaLeuAlaVal 22
 |||||
 Db 65 GGTCACAGCTGCTG-----CTCTCTACTACCCACCTCCCTGGCTCTG 112
 Qy 23 AlaProGlyProArgPheLeuValThrAlaProGlyLeileArg----- 37
 |||||
 Db 113 GGG---AGTCCCAGTACTATCATCACCACCAACATCTGGCTGGAGAGCGAGGAG 169
 Qy 38 -----ProGlyGlyAsnValThrileGlyValGluLeuLeu 49
 |||||
 Db 170 ACCATGCTGTGAGGCCACGACGCGCAAGGGATGTTCCAGTCACTGTTACTGCCAC 229
 Qy 50 GluHis-----CysProSerGlnValThrValLysAlaGluLeuLeu 63
 |||||
 Db 230 GACTTCCAGGCAAAAAGTAGTCTCTCCAGTGAGAGACTGTCTGACCCCTGCCACC 289
 Qy 64 LysThrAlaSerAsnLeuThrValSerVal---LeuGluAlaGluGlyValPheGluLys 82
 |||||
 Db 290 AACACATGGGCAACGTCACCTTTCACGATCCAGCCCAACAGGAGTTCAAGTCAGAAAAG 349
 Qy 83 GlySerPheLysThrLeuThrLeuProSerLeuProLeuAsnSerAlaAspGluLeuTyr 102
 |||||
 Db 350 GGGGCAACAAAGTCTGTGACCTGTCAGGCC-----ACCTCGGGACCCAAAGTGTG 400

Qy 103 GluLeuArgValThrGlyArgThrGlnAspGluLeuLeuPheSerAsnSerThrArgLeu 122
 |||||
 Db 401 GAGAAGGTGGTGGTCTGAGCTGAGAGCGGGTACCTC----- 439
 Qy 123 SerPheGluThrLysArgLysValPheIleGlnThrAspLysAlaLeuTyrLysPro 142
 |||||
 Db 440 -----TTTATCCAGACAGAACAGACCATCTACACCCCT 472
 Qy 143 LysGlnGluValLysPheArgLysValThrLeuPheSerAspPheLysProTyrLysThr 162
 |||||
 Db 473 GGCTCCACAGTTCTCTATCGGATCTTCCACCTCAACCACAGCTGCTACCCGTGGCGG 532
 Qy 163 SerLeuAsnIleLeuLysAspProLysSerAsnLeuLeuGlnGln---TrpLeuSer 181
 |||||
 Db 533 ACGETCATGGTCAACATTTGAGAACCCGAGGACATCCGGTCAAGCAGGACTCTCTGTCT 592
 Qy 182 GlnGlnSerAspLeuGlyValLysSerLysThrPheGlnLeuSerSerHisProIleLeu 201
 |||||
 Db 593 TCTCAGAACAGCTTGGGCTTGTCCCTTGTCTTGGGACATCTCGGACTCGTCAACATG 652
 Qy 202 GlyAspTrpSerIleGlnValGlnValAsnAsp-----GlnThrTyrTyrGlnSer 218
 |||||
 Db 653 GGCCAGTGGAGATCCGAGCTTACTATGAAAACTCACACAGCAGGCTCTTCTCCACTGAG 712
 Qy 219 PheGlnValSerGluTyrValLeuProLysPheGluValThrLeuGln-----ThrPro 236
 |||||
 Db 713 TTTGAGTGAAGGAGTACGTCTGCCAGTTTCAGGTCATAGTGGAGCTTACAGAGAAA 772
 Qy 237 LeuTyrCysSerMetAsnSerLysHisLeuAsnGlyThrIleThrAlaLysTyrThrTyr 256
 |||||
 Db 773 TTCTACTACATCTATAACGAGAGGGCTGGAGGTCACCATCCGCCAGGTTCTCTCTAC 832
 Qy 257 GlyLysProValLysGlyAspValThrLeuThrPhe----- 268
 |||||
 Db 833 GGGAGAAAGTGGAGGAACTGCTTGTCTATCTTCGGGATCCAGGATCCGCAACAGAGG 892
 Qy 269 -----LeuProLeuSerPheTyrGlyLysLysAsn 279
 |||||
 Db 893 ATTTCCTGCTGATCCCTCAAGCGCATTCGATTGAGGATGGCTCGGGGAGGTTGTG 952
 Qy 280 IleThrLysThrPheLysIleAsnGlySerAlaAsnPheSerPheAsnAspGluGluMet 299
 |||||
 Db 953 CTGAGCCGAAAGTACTCTGTCAGCGGGTGCAGAACCCCGAGCAGAGACCTGTGTGGG 1012
 Qy 300 LysAsnValMetAspSerSerAsnGlyLeuSerGluTyrLeuAspLeuSerSerProgly 319
 |||||
 Db 1013 AAGTCTTGTAGTCTGCTGCC----- 1033
 Qy 320 ProValGluIleLeuThrThrValThrGluSerValThrGlyIleSerArgAsnValSer 339
 |||||
 Db 1034 -----ACGTCATCTTGCATCGACCTCAGCAGTGCATGTCAGGACGAGCGC 1078
 Qy 340 ThrAsnValPhePheLysGlnHisAspTyrIleleGluPhePheAspTyrThrVal 359
 |||||
 Db 1079 AGCGGGATCCCATCGTGACCTCTCCCTACCAGATCCACTTCACCAAGACACCCCAAGTAC 1138
 Qy 360 LeuLysProSerLeuAsnPheThrAlaThrValLysValThrArgAlaAspGlyAsn--- 378
 |||||
 Db 1139 TTCAAACACGAGATGCCCTTTGACCTCATGTGTCTGTCGACGACCCCTGATGGCTCTCA 1198
 Qy 379 -----GlnLeuThrLeuGluArgAsnAsnValIleThrValThrGlnArg 396
 |||||
 Db 1199 GCCTACCGAGTCCCGTGGCAGTCCAGGGCGGAGGACACTGTCGACTCTCTAACCCAGGGA 1258
 Qy 397 AsnTyrThrGluTyrTrpSerGlySerAsnSerGlyAsnGlnLysMetGluAlaValGln 416
 |||||
 Db 1259 GATGCGGTGGCCAAACTCAGCATCAACACACACCCCGCCAGAG----- 1303
 Qy 417 LysIleAsnTyrThrValProGlnSerGlyThrPheLysIleGluPheProIleLeuGlu 436
 |||||
 Db 1304 -----CCCTTGAGCATCAGGTGGCGCACGAGAACGAGGACTCTCG 1345

Qy	437	AspSerSerGluLeuGlnLeuLysAlaTyrPheLeuGlySerLysSerMetAlaVal	456
Db	1346	GAGCGAGCAG-----GCTACCAAGGACCATGCAGGCTCTG	1381
Qy	457	HisSerLeuPheLysSerProSerLysThrTyrIleGlnLeuLysThr-----	472
Db	1382	CCCTACAGCACCGGGGCAACTCCAACTTCCTCTCTCAGTGTACGTACACAG	1441
Qy	473	-----ArgAspGluAsnIleLysValGlySerProPheGluLeuValValSerGlyAsn	490
Db	1442	CTCAGACCCGGGAGAGCCCTCAACGTCACACTTCCTCTGCGAATGAGCCGCGCCACGAG	1501
Qy	491	LysArgLeuLysGluLeuSerTyrMetValValSerArgGlyGlnLeuValAlaValGly	510
Db	1502	GCCAAAGATCCGCTACTACCTACTCATGATCAAGCAAGGCGAGCTGTGTTGAAGCGCGGA	1561
Qy	511	Lys-----GlnAsnSerThrMetPheSerLeuThrProGluAsnSer	524
Db	1562	CGCCAGGTGCGAGAGCCCGGCAGGACCTGGTGGTGTGCGCTGTCCATCACCACCGCAC	1621
Qy	525	TrpThrProLysAlaCysValIleValTyrTyr-----IleGluAspAspGly	540
Db	1622	TTTCATCCCTCTCTTCCGCTGGTGGCGGTACTACACGCTGATCGGTGCCAGCGGCCAGAGG	1681
Qy	541	GluIleIleSerAspValLeuLysIleProValGln-----LeuVal	554
Db	1682	GAGTGGTGGCGACTCCGTTGGTGGAGCGTCAAGGACTCTCTCGTGGGCTCGCTGGTG	1741
Qy	555	PheLysAsnLysIleLysLeuTyrTrpSerLysValLysAlaGlu-----	569
Db	1742	GTAAAAAGCGC-----CAGTCAGAAACCCGCGACGCTGTA	1777
Qy	570	ProSerGluLysValSerLeuArgIleSerValThrGlnProAspSerIleValGlyIle	589
Db	1778	CCTCGGCAGCAGATGACCTGAAGATAGAGGTGACCACCGGGCCCGGGTGGTA---CTG	1834
Qy	590	ValAlaValAspLysSerValAsnLeuMetAsnAlaSerAsnAspIleThrMetGluAsn	609
Db	1835	GTGCGCTGGCAAGGGCGTGTTCGTCTGAATAAGAAAGAACAACTCGACGACAGGTAAAG	1894
Qy	610	ValValHisGluLeuGluLeuTyrAsnThrGlyTyrTyrLeuGlyMetPheMetAsnSer	629
Db	1895	ATTCTGGAGCGTGGGAGAGCGCAGACATCGGTGACACCCCGGCGAGTGGGAAGGATTAC	1954
Qy	630	PheAlaValPheGlnGluCysGlyLeuTrpValLeuThrAspAla-----	644
Db	1955	GC CGGTGTCTCTCCGACGCGAGGGCTGACCTTCACGACGACGATGCGCCACGACCGCC	2014
Qy	644	-----	644
Db	2015	CAGAGGCAGAACTTCACTGCCCGCAGCCGCGCGCGAGCGCTTCCGTGCAGCTC	2074
Qy	645	-----AsnLeuThrLysAspTyrIle	651
Db	2075	ACGGAGAAGCGAATGCACAAGTCGGCAAGTACCCCAAGAGAGCTGCGCAAGTCTCGCGAG	2134
Qy	652	AspGlyValTyrAspAsn-----AlaGluTyrAlaGluArgPheMetGlu	666
Db	2135	GAUGCATGGGGAGAAACCCCATGAGGTTCTCTGTCGCCAGCGCGGACCCGCTTTCATCTCC	2194
Qy	667	GluAsnGlu-----GlyHisIleValAspIleHis	676
Db	2195	CTGGGCGAGGGGTGCAGAAGAGTCTTCTCGACTGTGCGAACTACATCAGAGCTGCGCG	2254
Qy	677	-----AspPheSerLeu	680
Db	2255	CGGCAGCACGCGGGCGACGCCACTCTGGGCTGGCCAGGAGTAACCTGTGATGAGGACATC	2314
Qy	681	GlySerSerProHisVal-----ArgLysHisPheProGluThrTrpIleTrp-----	696
Db	2315	ATTGCAGAAGAGAACATCGTTTCCCGAAGTGAGTTCACAGAGAGCTGGCTGTGGAACGTT	2374
Qy	697	-----LeuAspThrAsnMetGlyTyrArgIleTyr	706

Db	2375	GAGGACTTTGAAAGAGCCACCCGAAATAATGGAAATCTCTACGAAGCTC-----	2419
Qy	707	GlnGluPheGluValThrValProAspSerIleThrSerTrpValAlaThrGlyPheVal	726
Db	2420	-----ATGAATATATTTTTGAAAGACTCCATCACCACGTGGGAGATTCTGGCTGTGAGC	2473
Qy	727	IleSerGluAspLeuGlyLeuThrThrThrProValGlnLeuGlnAlaPheGln	746
Db	2474	ATGTCGACAGAAAGGATC---TGTGTGGCAGACCCCTTCGAGGTGACAGTAATGCAC	2530
Qy	747	ProPhePheIlePheLeuAsnLeuProTyTrSerValIleArgGlyGluGluPheAlaLeu	766
Db	2531	GACTTCTTCATGCACCTGGCGCTACCTACTCTGTGTTCGAAACGAGCAGGTGGAATC	2590
Qy	767	GluIleThrIlePheAsnTyLeuLysAspAlaThrGluValLysValIleIleGlu---	785
Db	2591	CGAGCCCTTCTTACAATTAC---CGCGAAGAACAGAGCTCAAGGTGAGGGTGAACCTA	2647
Qy	786	--LysSerAspLysPheAspIleLeuMetThrSerSerGluIleAsnAlaThrGlyHis	804
Db	2648	CTCCACAACTCCAGCTTCTCGACGCTGGCCACCAACAGAGG-----CGTCAC	2695
Qy	805	GlnGlnThrLeuLeuValProSerGluAspGlyAlaThrValLeuPheProIleArgPro	824
Db	2696	CAGCAGACCATAACCATCCCCCAAGTCTCGTTGTTCGTTCCATATGTCATCGTGC	2755
Qy	825	-----ThrHisLeuGlyGluIleProIleThrValThrAlaLeuSerProThrAlaSer	842
Db	2756	CTAAGACCGCGCTCGAGGAAGTGAAGTCAAGCGTCTGTCTTACCATCATTTTCATCAGT	2815
Qy	843	AspAlaValThrGlnMetIleLeuValLysAlaGluGlyIleGluLysSerTyrsGln	862
Db	2816	GACGGTGTACGGAAGTCCCTGAAGTCTGCCGGAAGGAATCAGATGAACAAACTGTG	2875
Qy	863	SerIleLeuLeuAspLeuThrAspAsnArgLeu-----GlnSerThrLeuLysThrLeu	880
Db	2876	GCTGTT---CGCACCTCGATCCAGAACGCTCGGCCGCTGAAGGAGTGCAGAAAGAG---	2929
Qy	881	SerPheSerPheProProAsnThrVal-----ThrGlySerGluArg	894
Db	2930	-----CACATCCACTGCAGACCTCAGTACCAAGTCCCGACACCGAGTCTGAGACC	2983
Qy	895	-----ValGlnIleThrAlaIleGlyAspValLeuGlyProSerIleAsnGly---	910
Db	2984	AGAATTCTCTGTAAGGACCCAGTGGCCACCATGACAGAGATCGCTGACGCGGAA	3043
Qy	911	--LeuAlaSerLeuIleArgMetProTyGlyCysGlyGluGlnAsnMetIleAsnPhe	929
Db	3044	CGGCTGAAGCACCTCATTTGACCCCTCGGGCTGCGGGAACAGAACATGATCGGCATG	3103
Qy	930	AlaProAsnIleTyrlleLeuAspTyTrLeuThrLysLysGlnLeuThrAspAsnLeu	949
Db	3104	ACGCCCCAGCTCATCGTGTGCATTACCTGGATGCAAAACGGAGCAGTGGGAGAAGTTCGGC	3163
Qy	950	LysGluLys-----AlaLeuSerPheMetArgGlnGlyTyTrGlnArgGluLeuLeu	966
Db	3164	CTAGAGAAGCGGAGGGGGCTTTGGAGCTCATCAAGAAGGGGTACACCAGCAGCTGGCC	3223
Qy	967	TyrGlnArgGluAspGlySerPheSerAlaPheGlyAsnTyTrAspProSerGlySerThr	986
Db	3224	TTCAGACAACCCAGCTCTGCTTTTGGGCGCTTCGTGAAACGGGCACCC-----AGCACC	3277
Qy	987	TrpLeuSerAlaPheValLeuArgCysPheLeuGluAlaAspProTyrlleAspIleAsp	1006
Db	3278	TGGCTGACCGCCTACGTGGTCAAGGTCTTCTCTCGCTGTCAACCTCATCGCCATCGAC	3337
Qy	1007	GlnAsnValLeuHisArgThrTyTrThrTrpLeu---LysGlyHisGlnLysSerAsnGly	1025
Db	3338	TCCCAAGTCTCTGCGGGGCTGTTAATGGCTGATCTCTGGAGAAGCAGAAAGCCGACGG	3397
Qy	1026	GluPheTrpAspProGlyArgValIleHisSerGluLeuGlnGlyGly-----	1041

Db 3398 GTCTTCAGAGAGATCGCCCGGTATACACCAAGAAATGATTGGTGGATTACGGAAACAC 3457
QY AsnLysSerProValThrLeuThrAlaTyrIleValThrSerLeuLeuGlyTyrArgLys 1061
Db 3458 AACGAGAAACATGCGCCCTCAGCGCTTGTTCATCTCGTG----- 3502
QY 1062 TyrGlnProAsnIleAspVal---GlnGluSerIleHis----- 1073
Db 3503 ---CAGGAGGCTAAAGATATTTCCGAGGAGCAGGTCAACAGGCTGCCAGGAGCATCACT 3559
QY 1074 -----PheLeuGluSerGluPheSerArgGlyIleSerAspAsnTyrThrLeu 1089
Db 3560 AAAGCAGGAGACTTCTTGAAGCAACTAC--ATGAACCTACAGAGATCCTACACTGTG 3616
QY 1090 AlaLeuIleThrTyrAlaLeuSerSerValGlySerProLysAlaLysGluAlaLeuAsn 1109
Db 3617 GCATTCGTGCTATGCTCTGGCCAGATGGCAGGCTGAAGGGGCTCTTCTTAACAAA 3676
QY 1110 MetLeuThrTrpArgAlaGluGlnGluGlyGlyMetGlnPheTrpValSerSerGluSer 1129
Db 3677 TTTCTGACC-----ACAGCC 3691
QY 1130 LysLeuSerAspSerTrpGln-----ProArgSerLeuAspIleGluValAlaAla 1146
Db 3692 AAAGATAAGAACCGCTGGGAGGACCTGGTAAGCAGCTCTACAACGTGGAGGCCACATCC 3751
QY 1147 TyrAlaLeuLeuSerHisPheLeuGlnPheGlnThrSerGluGlyIle---ProIleMet 1165
Db 3752 TATGCCCTCTTGCC---CTACTGCAGCTAAAGACTTTGACTTTGTGCTCCCGTCGTG 3808
QY 1166 ArgTrpLeuSerArgGlnArgAsnSerLeuGlyGlyPheAlaSerThrGlnAspThrThr 1185
Db 3809 CGTTGCTCAATGAACAGAGATACTACGGTGGTGGTATGGCTCTACCCAGGCCACCTTC 3868
QY 1186 ValAlaLeuLysAlaLeuSerGluPheAlaAla---LeuMetAsnThrGluArgThrAsn 1204
Db 3869 ATGGTGTTCAGACCTTGGCTCAATACCAAAAGAGCCCTGACCCACCAAGCACTGAAC 3928
QY 1205 IleGlnValThrValThrGlyProSerSer-----ProSerProLeu 1218
Db 3929 CITGATGTGTCCTCCAACTGCCCGCCG-CAGCTCAAGATCACCCACCGTATCCACTG 3987
QY 1219 AlaValValGlnProMetAlaVal-----Asn-IleSe 1229
Db 3988 GGAATCTGCCAGCTCTCGATCAGAGACCAAGAAATGAGGGTTTCACAGTCAC 4047
QY 1229 rAlaAsnGlyPheGlyPheAlaIleCysGlnLeuAsnValValTyrAsnValIleAsn 1249
Db 4048 AGCTGAAGAAAGGCAAGGCCACCTTGTGGTGGTGACAATGTACCATGTCTAAGGCCAA 4107
QY 1249 rGlySerSerArgArgArgSerIleGlnAsnGlnGluAlaPheAspLeuAspValAl 1269
Db 4108 AGATCAACTCACTGTAAATAA-----TTGCACTCAAGTCTAC 4146
QY 1269 aVal-----LysGluAsnLysAspLeuAsnHisValAspLe 1282
Db 4147 CATAAACCAGCACCGGAAACAGAAAGAGCCCTCAGGATGCCAAGACATCATGCTCT 4206
QY 1282 uAsnValCysThrSerPheSerGlyProGlyArgSerGlyMetAlaLeuMetGluValAs 1302
Db 4207 TGAGATCTGACAGGTACCGGGAGACCCAGGATGCCATATGCTATATTTGGACATATC 4266
QY 1302 nLeuLeuSerGlyPheMetValProSerGlu-----AlaIleSerLeuSe 1317
Db 4267 CATGATGACTGGCTTTGTCTCCAGACAGATGACCTGAAGCAGCTGGCCAAATGGTTGA 4326
QY 1317 rGluThrValLysValGluTyr-----AspHisGlyLysLeuAsnLe 1332
Db 4327 CAGATACATCTCAAGTATGAGTGGACAAAGCCTTCTCCGATAGGAAACACCTCATCAT 4386
QY 1332 uTyrLeuAspSerValAsnGluThrGln---PheCysValAsnIleProAlaValArgAs 1351
Db 4387 CTACCTGGACAAGGCTCACACTCTGAGGATGACTGTCTAGCTTTTCAAGTTCCACCAATA 4446

QY 1351 nPheLysValSerAsnThrGlnAspAlaSerValSerIleValAspTyrTyrGluProAr 1371
Db 4447 CTTTAATGTAGAGCTTATCCAGCTGGAGCAGTCAAGTCTTACGCTATTACAACTGGA 4506
QY 1371 gArgGlnAlaValArgSerTyrAsnSerGluVal-----LysLeuSerSerCysAs 1388
Db 4507 GGAAAGCTGTACCGGTTCTACCATCCGGAAGAGGAGATGGAAGCTGAACAAG----- 4561
QY 1388 pLeuCysSerAspValGlnGlyCysArgProCysGluAsp 1401
Db 4562 -CTCTGCCGTGAT---GAACGTGTCGGCTGTGCTGAGGAG 4597

RESULT 7

US-09-132-271-2
; Sequence 2, Application US/09132271
; Patent No. 6221657
; GENERAL INFORMATION:
; APPLICANT: Harrison, Richard Alexander
; APPLICANT: Farries, Charles Timothy
; TITLE OF INVENTION: MODIFIED HUMAN C3 PROTEINS
; NUMBER OF SEQUENCES: 2
; CORRESPONDENCE ADDRESS:
; ADDRESS: HALE AND DORR LLP
; STREET: 60 State Street
; CITY: Boston
; STATE: MA
; COUNTRY: United States of America
; ZIP: 02109
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA: US/09/132,271
; FILING DATE:
; CLASSIFICATION:
; PRIOR APPLICATION DATA: US/08/793,126
; APPLICATION NUMBER: US/08/793,126
; FILING DATE: 07-FEB-1997
; ATTORNEY/AGENT INFORMATION:
; NAME: Baker, Hollie L.
; REGISTRATION NUMBER: 31,321
; REFERENCE/DOCKET NUMBER: 102286.377
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (617) 526-6000
; TELEFAX: (617) 526-6000
; INFORMATION FOR SEQ ID NO: 2:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 5056 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: cDNA
US-09-132-271-2

Alignment Scores:
Pred. No.: 1,2e-89 Length: 5056
Score: 931.00 Matches: 381
Percent Similarity: 40.88% Conservative: 287
Best Local Similarity: 23.32% Mismatches: 609
Query Match: 12.67% Indels: 358
DB: 3 Gaps: 63

US-10-020-095-4 (1-1428) x US-09-132-271-2 (1-5056)

QY 3 GlyProProLeuLeuThrAlaAlaHisLeuLeuCysValCysThrAlaAlaLeuAlaVal 22
Db 65 GGTCCAGCGCTGCTG-----CTCTGCTACTACCCACCTCCCTGCTGCTG 112
QY 23 AlaProGlyProArgPheLeuValThrAlaProGlyIleIleArg----- 37

QY 652 AspGlyValTyrAspAsn-----AlaGluTyrAlaGluArgPheMetGlu 666
Db 2135 GACGGCATCGGGAGAACCCCATGAGTTCTCGTGCACGGCGGACCGCTTCATCTCC 2194
QY 667 GluAsnGlu-----GlyHisIleValAspIleHis 676
Db 2195 CTGGCGGAGCGGTGCAAGAGTCTTCCTGAGCTGTGCAACTACATCAGAGCTCGGG 2254
QY 677 -----AspPheSerLeu 680
Db 2255 CGGCAGCAGCGCGGGCCAGCCACCTGGCGCTGGCCAGGAGTAACCTGGATCAGGACATC 2314
QY 681 GlySerSerProHisVal-----ArgLysHisPheProGluThrTrpIleTrp----- 696
Db 2315 ATTGCAGAGAGAACATCGTTTCCGAGTAGTTCCTCCAGAGCTGCGGTGGAACGTT 2374
QY 697 -----LeuAspThrAsnMetGlyTyrArgIleTyr 706
Db 2375 GAGGACTTGAAGAGCCACCGAAAAATGGAATCTCTACGAGCTC----- 2419
QY 707 GlnGluPheGluValThrValProAspSerIleThrSerTrpValAlaThrGlyPheVal 726
Db 2420 -----ATGAATATATTTTGAAGAGACTCCATCACCAGCTGGGAGATTCTGGCTGTGAGC 2473
QY 727 IleSerGluAspLeuGlyLeuThrThrThrProValGlnGluAlaPheGln 746
Db 2474 ATGTCGAGCAAGAAAGGATC-----TGTGTGGAGACCCCTTCAGGTGCACGTAATGCGAG 2530
QY 747 ProPhePheIlePheLeuAsnLeuProTyrSerValIleArgGlyGlnGluPheAlaLeu 766
Db 2531 GACTTCTTCATCGACCTGCGGTACCTACTCTGTGTTGTCGAACAGCAGAGGTGGAATC 2590
QY 767 GluIleThrIlePheAsnTyrLeuLysAspAlaThrGluValLysValIleGlu----- 785
Db 2591 CGAGCGGTCTCTACAAATTAC-----CGCAGAACCAAGAGCTCAAGGTGAGGTGGAACATA 2647
QY 786 ---LysSerAspLysPheAspIleLeuMetThrSerSerGluIleAsnAlaThrGlyHis 804
Db 2648 CTCACATCCAGCTTCTCGACCTTGGCCACCAACAGAGG-----CGTCAC 2695
QY 805 GlnGlnThrLeuLeuValProSerGluAspGlyAlaThrValLeuPheProIleArgPro 824
Db 2696 CAGCAGACCAATAACATCCCGCCCAAGTCTCGTTGTCTCCATATGTCATCGTGGCG 2755
QY 825 -----ThrHisLeuGlyGluIleProIleThrValThrAlaLeuSerProThrAlaSer 842
Db 2756 CTAAGACCGCGCTGCAGGAAGTGAAGTCAAGCTGCTGTCTACCATCATTTTCACAGT 2815
QY 843 AspAlaValThrGlnMetIleLeuValLysAlaGluGlyIleGluLysSerTyrSerGln 862
Db 2816 GACGGTGTGAGGAAGTCCCTGAAGTGTGCGCAGAGGAATCAGAATGAACAAACTGTG 2875
QY 863 SerIleLeuLeuAspLeuThrAspAsnArgLeu-----GlnSerThrLeuLysThrLeu 880
Db 2876 GCTGTT---CGCACCTTGGATCCAGAACCGCTGGCGCGTGAAGAGTGCAGAAAGAG--- 2929
QY 881 SerPheSerPheProAsnThrVal-----ThrGlySerGluArg 894
Db 2930 -----GACATCCACCTGAGACCTCAGTGAACCAAGTCCCGGACCGAGCTGTGAGACC 2983
QY 895 -----ValGlnIleThrAlaIleGlyAspValLeuGlyProSerIleAsnGly--- 910
Db 2984 AGAATTCCTCTGCAAGGAGACCCAGTGGCCAGATGACAGAGGATGCCGTGCGACGGAA 3043
QY 911 ---LeuAlaSerIleIleArgMetProTyrGlyCysGlyGlnGlnAsnMetIleAsnPhe 929
Db 3044 CGGCTGAAGACCTCATGTGACCCCTCGGGCTGCGGGGAACAGACATGATCGGCATG 3103
QY 930 AlaProAsnIleTyrIleLeuAspTyrLeuThrLysLysGlnLeuThrAspAsnLeu 949
Db 3104 ACGCCACGGTCACTCGTGTGCTTACTCTGATGAACCGGAGCAGTGGGAGAGTTCCGC 3163
QY 950 LysGluLys-----AlaLeuSerPheMetArgGlnGlyTyrGlnArgGluLeuLeu 966

Db 3164 CTAGAGAAAGCGCGAGGGCGCTTGGAGCTCATCAAGAGGGGTACACCCAGCAGCTGCC 3223
QY 967 TyrGlnArgGluAspGlySerPheSerAlaPheGlyAsnTyrAspProSerGlySerThr 986
Db 3224 TTCAGACAAACCCAGCTCTGCGCTTTCGGGCTTCGTGAACCGGCACCC-----AGCAC 3277
QY 987 TrpLeuSerAlaPheValLeuArgCysPheLeuGluAlaAspProTyrIleAspIleAsp 1006
Db 3278 TGGCTGACCGCTACGTGGTCAAGTCTTCTCTGCTGTCTCAACCTCATCGCATCGAC 3337
QY 1007 GlnAsnValLeuHisArgThrTyrThrTrpLeu---LysGlyHisGlnLysSerAsnGly 1025
Db 3338 TCCCAAGTCTCTCGGGCGCTGTTAAATGGTGTATCTCTGGAGAAGCAGAACCCGACGG 3397
QY 1026 GluPheTrpAspProGlyArgValIleHisSerGluLeuGlnGlyGly----- 1041
Db 3398 CTCCTCCAGGAGGATGCGCCGCTGATACCAACAAGAAATGATTGGTGGATTACGGAACAAC 3457
QY 1042 AsnLysSerProValThrLeuThrAlaTyrIleValThrSerLeuLeuGlyTyrArgLys 1061
Db 3458 AACGAGAAAGACATGCGCCCTCAGCGCTTGTGTTCTCATCTCGCTG----- 3502
QY 1062 TyrGlnProAsnIleAspVal---GlnGluSerIleHis----- 1073
Db 3503 ---CAGGAGGCTAAAGATATTTGCGAGGAGCAGGTCAACAGCTGCCAGGCGACATCACT 3559
QY 1074 -----PheLeuGluSerGluPheSerArgGlyIleSerAspAsnTyrThrLeu 1089
Db 3560 AAAGCAGGAGACTTCTTGAAGCCCAACTAC---ATGAACCTACAGAGATCTCTACTGTG 3616
QY 1090 AlaLeuIleThrTyrAlaLeuSerSerValGlySerProLysAlaLysGluAlaLeuAsn 1109
Db 3617 GCCATTGTGCTATGCTCTGCCCCAGATGGCAGGTGAAGGGCCCTCTTCTTAACAAA 3676
QY 1110 MetLeuThrTrpArgAlaGluGlnGlyGlyMetGlnPheTrpValSerSerGluSer 1129
Db 3677 TTTCTGACC-----ACAGCC 3691
QY 1130 LysLeuSerAspSerTrpGln-----ProArgSerLeuAspIleGluValAlaAla 1146
Db 3692 AAAGATAGAACCGCTGGAGAGACCTGTAAGAGCTCTACAGCTGAGGAGCCACATCC 3751
QY 1147 TyrAlaLeuLeuSerHisPheLeuGlnPheGlnThrSerGluGlyIle---ProIleMet 1165
Db 3752 TATGCCCTCTTGCC---CTACTGCAGCTAAAGACTTGACTTTGTGCTCCCTCCCTCGTG 3808
QY 1166 ArgTrpLeuSerArgGlnArgAsnSerLeuGlyGlyPheAlaSerThrGlnAspThrThr 1185
Db 3809 CGTTCGCTCAATGAACAGAGATACACGCTGTGCTATGGCTCTTACCAGCCACCTTC 3868
QY 1186 ValAlaLeuLysAlaLeuSerGluPheAlaAla---LeuMetAsnThrGluArgThrAsn 1204
Db 3869 ATGGTGTCCAAGCTTGGCTCAATACCAAGGAGCGCCCTGACCCAGCAAGCACTGAAC 3928
QY 1205 IleGlnValThrValThrGlyProSerSer-----ProSerProLeu 1218
Db 3929 CTTGTATGTCTCCCTCCAACCTGCCAGCGG-CAGCTTCCAAGATCACCCACCGTATCCACTG 3987
QY 1219 AlaValValGlnProMetAlaVal-----Asn-IleSer 1229
Db 3988 GGAATCTGCCACCTCTCGCGATCAGAGACCAAGGAAATAGGGTTTCACAGTCAAC 4047
QY 1229 rAlaAsnGlyPheGlyPheAlaIleCysGlnLeuAsnValValTyrAsnValLysAlaSer 1249
Db 4048 AGCTGAAGGAAAGCCCAAGGACCCCTTGTGCGTGTGACAATGTACCATGTCTAAGGCCAA 4107
QY 1249 rGlySerSerArgArgArgSerIleGlnAsnGlnGluAlaPheAspLeuAspValAla 1269
Db 4108 AGATCAACTCACTGTATAATAA-----TTTCAGCTCAAGCTCAC 4146
QY 1269 aVal-----LysGluAsnLysAspAspLeuAsnHisValAspLe 1282

Db 4147 CATAAACACGACCGGAAACAGAAAGAGCGCTCAGGATGCCCAAGACACTATGATCCT 4206
 QY 1282 uasnValCysThrSerPheSerGlyProGlyArgSerGlyMetAlaLeuMetGluValAs 1302
 Db 4207 TGAGATCTGTACCAAGGTACCGGGAGACACGAGATGCCACTATGTCTATATTGGACATATC 4266
 QY 1302 nLeuLeuSerGlyPheMetValProSerGlu-----AlaIleSerLeuSe 1317
 Db 4267 CATGATGACTGCTTGTCTCAGACACAGATGACCTGAGCAGCTGCCCAATGGTGTGA 4326
 QY 1317 rGluThrValLysLysValGluTyr-----AspHisGlyLysLeuAsnLe 1332
 Db 4327 CAGATACATCTCCAAGTATGAGTGGACAAAGCCCTTCCGATAGGAACACCCCTCATCAT 4386
 QY 1332 uTyrLeuAspSerValAsnGluThrGln---PheCysValAsnIleProAlaValArgAs 1351
 Db 4387 CTACTGTGACAAAGTCTCACACTCTGAGGATGACTGTCTAGCTTTCAAAGTTCCACCAATA 4446
 QY 1351 nPheLysValSerAsnThrGlnAspAlaSerValSerIleValAspTyrTyrGluProAr 1371
 Db 4447 CTTTAATGTAGAGCTTATCCAGCCTGGAGCAGTCAAGTCTACGCCTATTACAACCTGGA 4506
 QY 1371 gArgGluAlaValArgSerTyrAsnSerGluVal-----LysLeuSerSerCysAs 1388
 Db 4507 GGAAAGCTGTACCCGGTCTTACCATCCGGAAGAGGAGGATGGAAAGCTGAACAAG----- 4561
 QY 1388 pLeuCysSerAspValGlnGlyCysArgProCysGluAsp 1401
 Db 4562 -CTCTGCCGTGAT---GAACTGTGCCCTGTGCTGAGGAG 4597
 RESULT 8
 US-09-142-334-23
 ; Sequence 23, Application US/09142334
 ; Patent No. 6268485
 ; GENERAL INFORMATION:
 ; APPLICANT: Parries, Timothy C.
 ; APPLICANT: Harrison, Richard A.
 ; TITLE OF INVENTION: Down-Regulation Resistant C3 Convertase
 ; FILE REFERENCE: 4-30443/A/INU/PCF
 ; CURRENT APPLICATION NUMBER: US/09/142,334
 ; CURRENT FILING DATE: 1999-04-15
 ; EARLIER APPLICATION NUMBER: PCT/GB97/00603
 ; EARLIER FILING DATE: 1997-03-04
 ; NUMBER OF SEQ. ID NOS: 35
 ; SOFTWARE: PatentIn Ver. 2.0
 ; SEQ ID NO 23
 ; LENGTH: 5067
 ; TYPE: DNA
 ; ORGANISM: Homo sapiens
 US-09-142-334-23
 Alignment Scores:
 Pred. No.: 1,2e-89 Length: 5067
 Score: 931.00 Matches: 381
 Percent Similarity: 40.88% Conservative: 287
 Best Local Similarity: 23.32% Mismatches: 609
 Query Match: 12.67% Indels: 358
 DB: 3 Gaps: 63
 US-10-020-095-4 (1-1428) x US-09-142-334-23 (1-5067)
 QY 3 GlyProProLeuLeuThrAlaAlaHisLeuLeuCysValCysThrAlaAlaLeuAlaVal 22
 Db 76 GGTCCAGCTGTG-----CTCCTGCTACTAACCCACCTCCCTCGCTGTG 123
 QY 23 AlaProGlyProArgPheLeuValThrAlaProGlyIleArg----- 37
 Db 124 GGG---AGTCCCATGTACTATCATCACCCCAACATCTTGGCGTGGAGCGAGGAG 180
 QY 38 -----ProGlyGlyAsnValThrIleGlyValGluLeuLeu 49
 Db 181 ACCATGGTGTGGAGGCCCAAGCGCGCAAGGGAGTGTCCAGTCACTGTTACTGTCCAC 240

QY 50 GluHis-----CysProSerGlnValThrValLysAlaGluLeuLeu 63
 Db 241 GACTTCCCGAGGCAAAAACTAGTGTCTCCAGTGAGAAAGACTGTGCTGACCCCTGCCACC 300
 QY 64 LysThrAlaSerAsnLeuThrValSerVal---LeuGluAlaGluGlyValPheGluLys 82
 Db 301 AACACATGGGCAACGTCACCTTCAGGATCCAGCCACAGGAGTTCAGTCAAGTCAAGAAAG 360
 QY 83 GlySerPheLysThrLeuThrLeuProSerLeuProLeuAsnSerAlaAspGluIleTyr 102
 Db 361 GGGCGCAACAAGTTGTCACCGTGCAGGCC-----ACCTTCGGGACCAAGTGTGTG 411
 QY 103 GluLeuArgValThrGlyArgThrGlnAspGluIleLeuPheSerAsnSerThrArgLeu 122
 Db 412 GGAAGGTGGTGTCTGCTGCTGAGCTGAGCGCGGTACCTC----- 450
 QY 123 SerPheGluThrLysArgIleSerValPheIleGlnThrAspLysAlaLeuTyrLysPro 142
 Db 451 -----TTCAATCAGACAGACAAAGACCATCTACACCCCT 483
 QY 143 LysGlnGluValLysPheArgIleValThrLeuPheSerAspPheLysProTyrLysThr 162
 Db 484 GCCTCCACAGTTCCTATCCGATCTTACCGTCAACCAAGCTGCTACCGTGGCGCG 543
 QY 163 SerLeuAsnIleLeuIleLysAspProLysSerAsnLeuIleGlnGln---TrpLeuSer 181
 Db 544 ACGGTCAATGTCACATTGAGAACCGGAGGCATCCGGTCAAGCAGGAGTCTCTGTCT 603
 QY 182 GlnGlnSerAspLeuGlyValIleSerLysThrPheGlnLeuSerSerHisProIleLeu 201
 Db 604 TCTCAGAACCAAGTGGCGTCTGCTCCCTGCTGGGACATTCGCGAACTCGTCAACATG 663
 QY 202 GlyAspTrpSerIleGlnValGlnValAsnAsp-----GlnThrTyrTyrGlnSer 218
 Db 664 GGCCAGTGGAGATCCGAGCTACTATGAAACTCACCACAGCAGGTCTCTCCACTGAG 723
 QY 219 PheGlnValSerGluTyrValLeuProLysPheGluValThrLeuGln-----ThrPro 236
 Db 724 TTTGAGTGAAGAGTACGTCTGCCAGTGTTCGAGGTTCAGGTGATAGTGGAGCCTACAGAAA 783
 QY 237 LeuTyrCysSerMetAsnSerLysHisLeuAsnGlyThrIleThrAlaLysTyrTyr 256
 Db 784 TTCTACTACATCTATACAGAGAGGCTGAGGTCACTACCCGCGAGGTTCCTCTAC 843
 QY 257 GlyLysProValLysGlyAspValThrLeuThrPhe----- 268
 Db 844 GGAAGAAAGTGGAGGAACTGCTCTTCGATCTTCGGATCCAGGATCGGAACAGG 903
 QY 269 -----LeuProLeuSerPheTrpGlyLysLysLysAsn 279
 Db 904 ATTTCCCTGCTGAATCCCTCAAGCGCATTCGATTCGAGTTCGAGTTCGCGGAGGTGTG 963
 QY 280 IleThrLysThrPheLysIleAsnGlySerAlaAsnPheSerPheAsnAspGluMet 299
 Db 964 CTGAGCCGGAAGGTACTGCTGAGCGGGTGCAGAACCCCGAGCAGAGAGACTGTGTGGG 1023
 QY 300 LysAsnValMetAspSerSerAsnGlyLeuSerGluTyrLeuAspLeuSerSerProGly 319
 Db 1024 AAGTCTTTGTACGTGTCTGCC----- 1044
 QY 320 ProValGluIleLeuThrThrValThrGluSerValThrGlyIleSerArgAsnValSer 339
 Db 1045 -----ACCGTCATCTTCACCTCAGGAGTGCATGTCGAGCAGAGCGC 1089
 QY 340 ThrAsnValPhePheLysGlnHisAspTyrIleIleGluPhePheAspTyrThrVal 359
 Db 1090 AGCGGGATCCCATCGTGTGACCTCTCTCCCTACCATCTCCACCAAGACACCCCAAGTAC 1149
 QY 360 LeuLysProSerLeuAsnPheThrAlaThrValLysValThrArgAlaAspGlyAsn--- 378
 Db 1150 TTCAACAGGAATGCCCTTTGACCTCATGTTGTGTGACGAACCCCTGATGTCTCCA 1209
 QY 379 -----GlnLeuThrLeuGluAlaArgAsnValValIleThrValThrGlnArg 396

Db	1210	GCCTACGAGTCCCGTGGCAGTCCAGGCGAGACACTGTGCAGTCTCTAACCCAGGGA	1269
Qy	397	AsnTyrThrGluTyrTrpSerGlySerAsnSerGlyAsnGlnLysMetGluAlaValGln	416
Db	1270	GATGGGTGGCCAACTACATCAACACACACCCAGCCAGAG	1314
Qy	417	LysIleAsnTyrThrValProGlnSerGlyThrPheLysIleGluPheProIleLeuGlu	436
Db	1315	-----CCCTTGAGCATCACGGTGGCAGCAAGAACAGCAGAGCTCTCG	1356
Qy	437	AspSerSerGluLeuGlnLeuLysAlaTyrPheLeuGlySerLysSerSerMetAlaVal	456
Db	1357	GAGGCAGAGCAG	1392
Qy	457	HisSerLeuPheLysSerProSerLysThrTyrIleGlnLeuLysThr	472
Db	1393	CCCTACAGACCGTGGGCACTCAACATTTACTGCTGCTCAGTGTAGTACAGAG	1452
Qy	473	-----ArgAspGluAsnIleLysValGlySerProPheGluLeuValValSerGlyAsn	490
Db	1453	CTCAGACCCCGGGAGACCCCTCAACAGTCACTTCTCTCGAATGACCGCGCCACGAG	1512
Qy	491	LysArgLeuLysGluLeuSerTyrMetValValSerArgGlyGlnLeuValAlaValGly	510
Db	1513	GCCAGATCCGCTACTACACTACCTACCTGATCATGACAAAGGCGAGGTGTGAAGCGGGA	1572
Qy	511	Lys-----GlnAsnSerThrMetPheSerLeuThrProGluAsnSer	524
Db	1573	CGCCAGGTGCGAGAGCCGCGCAGGACCTGGTGGTGTGCTGCCCTCCATCACCCAGAC	1632
Qy	525	TrpThrProLysAlaCysValIleValTyr	540
Db	1633	TTATCCCTTCTTCGCGCTGGTGGGTACTACAGCTGATCGTGGCAGCGCCAGAGG	1692
Qy	541	GluIleIleSerAspValLeuLysIleProValGln-----LeuVal	554
Db	1693	GAGTGGTGGCCGACTCCGCTGGTGGTGGAGTCAAGACTCTCTGCTGGGCTCGCTGGTG	1752
Qy	555	PheLysAsnLysIleLysLeuTyrTrpSerLysValLysAlaGlu-----	569
Db	1753	GTAAAGACCGC-----CAGTCAGAAACCGGCGACCTGTA	1788
Qy	570	ProSerGluLysValSerLeuArgIleSerValThrGlnProAspSerIleValGlyIle	589
Db	1789	CTTGGCGAGCAGATGACCTTGAAGATAGAGGTGACACCGGCGCCGGGTGGTA---CTG	1845
Qy	590	ValAlaValAspLysSerValAsnLeuMetAsnAlaSerAsnAspIleThrMetGluAsn	609
Db	1846	GTGCGCGTGACAAAGGCGGTCTGCTGCTGAATAAGAAAGAACAACTGACGCGAGTAAG	1905
Qy	610	ValValHisGluLeuGluLeuTyrAsnThrGlyTyrTyrLeuGlyMetPheMetAsnSer	629
Db	1906	ATCTGGGACGTGGTGGAGAGGCGACATCGGCTGCACCCCGGCGAGTGGGAAGGATTAC	1965
Qy	630	PheAlaValPheGlnGluCysGlyLeuTrpValLeuThrAspAla-----	644
Db	1966	GCCGCTCTCTCCGACGCGAGGCTGACCTTACAGAGCAGCAGTGGCCAGCAGACCGCC	2025
Qy	644	-----	644
Db	2026	CAGAGGCGAGAACTTCAGTGCCTGCGCAGCCGCGCGCGCGCGCTTCCGTCAGCTC	2085
Qy	645	-----AsnLeuThrLysAspTyrIle	651
Db	2086	ACGAGAGCGAATGGCAAGTCGGCAAGTACCCCAAGAGCTGCGCAAGTCTCGGAG	2145
Qy	652	AspGlyValTyrAspAsn-----AlaGluTyrAlaGluArgPheMetGlu	666
Db	2146	GACGGCATCGGGAGAAACCCCATGAGTTCGTGGCCAGCGCGGACCCGCTTTCATCTCC	2205
Qy	667	GluAsnGlu-----GlyHisIleValAspIleHis	676

Db	2206	CTGGCGAGGCGTGCAGAAAGGTCTTCTGTGACTGTGCAACTACATCACAGAGCTCGG	2265
Qy	677	-----AspPheSerLeu	680
Db	2266	CGGCAGCAGCGCGCGCCAGCCACTGTGGCTGCGCCAGGAGTAACCTGGATGAGACATC	2325
Qy	681	GlySerSerProHisVal-----ArgLysHisPheProGluThrTrpIleTrp	696
Db	2326	ATTGCAGAGAAGACATCGTTTCCGGAAGTGTCCAGAGAGCTGCTGTGAACGTT	2385
Qy	697	-----LeuAspThrAsnMetGlyTyrArgIleTyr	706
Db	2386	GAGGACTTGAAGACCCACCGAAATCTCTACGAAGCTC-----	2430
Qy	707	GlnGluPheGluValThrValProAspSerIleThrSerTrpValAlaThrGlyPheVal	726
Db	2431	-----ATGAATATATATTTTGAAGACTCCATCAACCGTGGAGATTCTGCGCTGAGC	2484
Qy	727	IleSerGluAspLeuGlyLeuThrThrThrProValGluLeuGlnAlaPheGln	746
Db	2485	ATGTCGGHCAAGAAAGGATC---TGTGTGCACACCCCTTCGAGGTACAGATATGACG	2541
Qy	747	ProPhePheIlePheLeuAsnLeuProTyrSerValIleArgGlyGluGluPheAlaLeu	766
Db	2542	GACTTCTTCACTGACCTCGGCTACCTTCTGTGTTCGAAACGACGAGGTGAAATC	2601
Qy	767	GluIleThrIlePheAsnTyrLeuLysAspAlaThrGluValLysValIleGlu---	785
Db	2602	CGAGCGTCTCTCAATATC---CGGCAGAACCAAGAGTCAAGGTGAGGTGAACTA	2658
Qy	786	---LysSerAspLysPheAspIleLeuMetThrSerSerGluIleAsnAlaThrGlyHis	804
Db	2659	CTCCACATCCAGCCCTCTGCAGCTGCGCCACCAAGAGG-----CGTCAC	2706
Qy	805	GlnGlnThrLeuLeuValProSerGluAspGlyAlaThrValLeuPheProIleArgPro	824
Db	2707	CAGCAGACATAACCATCCCGCCCAAGTCTCGTGTCCGTTCATATGTATCTGTCGG	2766
Qy	825	-----ThrHisLeuGlyLysIleProIleThrValThrAlaLeuSerProThrAlaSer	842
Db	2767	CTAAGACCGGCTGCAGAAAGTGAAGTCAAGGTGCTGTCTACCATCATTTTCATCAGT	2826
Qy	843	AspAlaValThrGlnMetIleLeuValLysAlaGluGlyIleGluLysSerTyrSerGln	862
Db	2827	GACGCTGTGAGAAAGTCCCTGAAAGTCTGTCGGAAGGAATCAGAATGAACAACTCTG	2886
Qy	863	SerIleLeuLeuAspLeuThrAspAsnArgLeu-----GlnSerThrLeuLysThrLeu	880
Db	2887	GCTGTT---CGCACCTTGATCCAGAACGCTTGGCCCTGAAGAGTCCAGAAAGAG---	2940
Qy	881	SerPheSerPheProAsnThrVal-----ThrGlySerGluArg	894
Db	2941	-----GACATCCACCTGCAGACCTCAGTACCAAGTCCCGGACACCGAGTCTGAGACC	2994
Qy	895	-----ValGlnIleThrAlaIleGlyAspValLeuGlyProSerIleAsnGly---	910
Db	2995	AGAATTTCTCTCAAGGAGCCCGAGTGGCCCGCAGATGACAGAGGATGCGCTGACCGGAA	3054
Qy	911	---LeuAlaSerLeuIleArgMetProTyrGlyCysGlyGluGlnAsnMetIleAsnPhe	929
Db	3055	CGGCTGAAGCAGCTCATTTGTGACCCCTCGGGCTCGGGGAACACAGATGATCGCATG	3114
Qy	930	AlaProAsnIleTyrIleLeuAspTyrLeuThrLysLysLysGlnLeuThrAspAsnLeu	949
Db	3115	ACGCCCACGCTCATCGCTGTGCAATTACCTGGATGAACGGGAGAGTGGGAGAGTTCGCG	3174
Qy	950	LysGluLys-----AlaLeuSerPheMetArgGlnGlyTyrGlnArgGluLeuLeu	966
Db	3175	CTAGAGAGCGGCGAGGCGCTTGGAGTCTATCAAGAGGGGTACACCCAGCAGCTGGCC	3234
Qy	967	TyrGlnArgGluAspGlySerPheSerAlaPheGlyAsnTyrAspProSerGlySerThr	986
Db	3235	TTTCAGACAAACCCAGCTCTGCTTTCGGGCTTTCGTGAACCGGGCACCC-----AGCACC	3288

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QY 987 TrpLeuSerAlaPheValLeuArgCysPheLeuGluAlaAspProTyrIleAspIleAsp 1006
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QY 1007 GlnAsnValLeuHisArgThrTyrThrTrpLeu---LysGlyHisGlnLysSerAsnGly 1025
DB 3349 TCCCAAGTCTCTCGGGGGCTGTTAAATGGCTGATCTCTGGAGAAGCAGAAAGCCGCGG 3408
QY 1026 GluPheTrpAspProGlyArgValIleHisSerGluLeuGlnGly----- 1041
DB 3409 GTCTTCAGGAGGATGCGCCGCTGATACACCAAGAAATGATGGTGATACCGAACAAC 3468
QY 1042 AsnLysSerProValThrLeuThrAlaTyrIleValThrSerLeuLeuGlyTyrArgLys 1061
DB 3469 AACGAGAAAGACATGGCCCTCAGCGCTTGTCTCTCATCTCGCTG----- 3513
QY 1062 TyrGlnProAsnIleAspVal---GlnGluSerIleHis----- 1073
DB 3514 ---CAGGAGGCTAAAGATATTGGAGGAGCAGGTCAACAGCTGCGCAGGCAATCACT 3570
QY 1074 -----PheLeuGluSerGluPheSerArgGlyIleSerAspAsnTyrThrLeu 1089
DB 3571 AAACGAGGAGACTTCTTGAAGCCAACTAC---ATGAACCTACAGAGATCCTACACTGTG 3627
QY 1090 AlaLeuIleThrTyrAlaLeuSerSerValGlySerProLysAlaLysGluAlaLeuAsn 1109
DB 3628 GCCATTGCTGGCTATGCTCTGGCCAGATGGCAGGTCAAGGGCTCTTCTTAACAA 3687
QY 1110 MetLeuThrTrpArgAlaGluGlnGlyGlyMetGlnPheTrpValSerSerGluSer 1129
DB 3688 TTTCTGACC----- 3702
QY 1130 LysLeuSerAspSerTrpGln-----ProArgSerLeuAspIleGluValAlaAla 1146
DB 3703 AAAGATAGAACCCCTGGAGGACCCTGGTAAAGCAGCTCTACACGTGGAGGCAATCC 3762
QY 1147 TyrAlaLeuLeuSerHisPheLeuGlnPheGlnThrSerGluGlyIle---ProIleMet 1165
DB 3763 TATGCCCTCTGGCC---CTACTGCAGTAAAGACTTTGACTTTGTGCTCCGCTCGTG 3819
QY 1166 ArgTrpLeuSerArgGlnArgAsnSerLeuGlyGlyPheAlaSerThrGlnAspThrThr 1185
DB 3820 CGTTGGCTCAATGAACAGAGATACCTACGGTGGTGGCTATGGCTCTACCCAGGCCACTTC 3879
QY 1186 ValAlaLeuLysAlaLeuSerGluPheAlaAla---LeuMetAsnThrGluArgThrAsn 1204
DB 3880 ATGGTGTTCAGAGCTTGGCTCAATACCAAGAGAGCCCTCACCACCAAGGAAGTGAAC 3939
QY 1205 IleGlnValThrValThrGlyProSerSer-----ProSerProLeu 1218
DB 3940 CTGATGTGTCCTCCAACTGCCAGCGC-CAGCTCAAGATCACCACCGATATCCACTG 3998
QY 1219 AlaValValGlnProMetAlaVal-----Asn-IleSe 1229
DB 3999 GGAATCTGCAGCTCTCTGGATCAGAGAGACCAAGAGAAATGAGGGTTTCACATCAC 4058
QY 1229 rAlaAsnGlyPheGlyPheAlaIleCysGlnLeuAsnValValTyrAsnValLysAlaSe 1249
DB 4059 AGCTGAAGGAAAGCCCAAGCCACTTGTGGTGGTGACAAATGATACCATGCTAAGGCCAA 4118
QY 1249 rGlySerSerArgArgArgSerIleGlnAsnGlnGluAlaPheAspLeuAspValAl 1269
DB 4119 AGATCAACTCACCTGTAATAA-----TTGACCTCAAGTCTAC 4157
QY 1269 aVal-----LysGluAsnLysAspAspLeuAsnHisValAspLe 1282
DB 4158 CATAAACACGACCGGAAACAGAAAGAGCCCTCAGGATGCCAAGAACACTATGATCCT 4217
QY 1282 uAsnValCysThrSerPheSerGlyProGlyArgSerGlyMetAlaLeuMetGluValas 1302
DB 4218 TGATCTGTACCAAGGTACCAGGGGACCAAGGATGCCACTATGCTATATATTTGACATATC 4277

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QY 1302 nLeuLeuSerGlyPheMetValProSerGlu-----AlaIleSerLeuSe 1317
DB 4278 CATGATGACTGGCTTTGCTCCAGACACAGATACCTGAAGCAGCTGGCCAAATGGTGTTGA 4337
QY 1317 rGluThrValLysLysValGluTyr-----AspHisGlyLysLeuAsnLe 1332
DB 4338 CAGATACATCTCCAAGTATGAGCTGGACAAAGCCCTTCTCCGATAGGAACCCCTCATCAT 4397
QY 1332 uTyrLeuAspSerValAsnGluThrGln---PheCysValAsnIleProAlaValArgAs 1351
DB 4398 CTACCTGACCAAGGCTCTCACACTCTGAGGATGACTGTCTAGCTTTCAAGTTCCACAAATA 4457
QY 1351 nPheLysValSerAsnThrGlnAspAlaSerValSerIleValAspTyrTyrGluProAr 1371
DB 4458 CTTTAAATGTAGAGCTTATCCAGCTGGAGCAGTCAAGTCTACGCCTATTACACCTGGA 4517
QY 1371 gArgGlnAlaValArgSerTyrAsnSerGluVal-----LysLeuSerSerCysAs 1388
DB 4518 GGAAAGCTGTACCCGGTTCTACCATCCGAAAGAGGAGGATGGAAGCTGAACAAG----- 4572
QY 1388 pLeuCysSerAspValGlnGlyCysAspProCysGluAsp 1401
DB 4573 -CTCTGCCGTGAT---GAACTGTCGCTGTGCTGAGGAG 4608

RESULT 9
US-09-566-921-107
; Sequence 107, Application US/09566921
; Patent No. 6682888
; GENERAL INFORMATION:
; APPLICANT: Loring, Jeanne F.
; APPLICANT: Tingley, Debora W.
; APPLICANT: Edwards, Carla M.
; TITLE OF INVENTION: GENES EXPRESSED IN ALZHEIMER'S DISEASE
; FILE REFERENCE: PA-0024 US
; CURRENT APPLICATION NUMBER: US/09/566,921
; CURRENT FILING DATE: 2000-05-05
; NUMBER OF SEQ ID NOS: 138
; SOFTWARE: PERL Program
; SEQ ID NO 107
; LENGTH: 5129
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: misc_feature
; OTHER INFORMATION: Incyte ID NO. 6682888 1000186.8
US-09-566-921-107

Alignment Scores:
Pred. No.: 1,58e-89 Length: 5129
Score: 930.00 Matches: 381
Percent Similarity: 40.88% Conservative: 287
Best Local Similarity: 23.32% Mismatches: 609
Query Match: 12.66% Indels: 358
DB: 4 Gaps: 63

US-10-020-095-4 (1-1428) x US-09-566-921-107 (1-5129)
QY 3 GlyProProLeuLeuThrAlaAlaHisLeuLeuCysValCysThrAlaAlaLeuAlaVal 22
DB 91 GGTCCACCGCTGCTG-----CTCCTGTCTACTAACCCACCTCCCTCGCTCTG 138
QY 23 AlaProGlyProArgPheLeuValThrAlaProGlyIleIleArg----- 37
DB 139 GGG---AGTCCCATGTACTCTATCATCACCCTCCCAACATCTGCGGCTGGAGGAGGAG 195
QY 38 -----ProGlyGlyAsnValThrIleGlyValGluLeu 49
DB 196 ACCATGGTGTGGAGGCCGCCAGCGCGCAAGGGGATGTTCCAGTCACTGTTACTGTCCAC 255
QY 50 GluHis-----CysProSerGlnValThrValLysAlaGluLeu 63
DB 256 GACTTCCAGCGCAAAAAAAGCTAGTGTCTGTCCAGTGAGAGACTGTGTGACCCCTGCCACC 315

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QY 64 LysThrAlaSerAsnLeuThrValSerVal---LeuGluAlaGluGlyValPheGluLys 82
Db 316 AACACATGGCCACGTCACCTTCAGATCCCAAGCAAGAGGAGTCAAGTCAGAAAG 375
QY 83 GlySerPheLysThrLeuThrLeuProSerLeuProLeuAsnSerAlaAspGluLeuTyr 102
Db 376 GGGCGCAACAGTTCGTGACCGTCAGGCC-----ACCTTCGGGACCCCAAGTGGTG 426
QY 103 GluLeuArgValThrGlyArgThrGlnAspGluLeuPheSerAsnSerThrArgLeu 122
Db 427 GAGAAGTGTGTGTGTCACCTTCACAGCGGTACCTC----- 465
QY 123 SerPheGluThrLysArgIleSerValPheIleGlnThrAspLysAlaLeuTyrLysPro 142
Db 466 -----TTTCATCCAGACACAGACCACTACACCCCT 498
QY 143 LysGlnGluValLysPheArgIleValThrLeuPheSerAspPheLysProTyrLysThr 162
Db 499 GGCTCCACAGTCTCTATCGATCTTCACCGTCAACACCAAGCTGTACCGTGGGCCG 558
QY 163 SerLeuAsnIleLeuIleLysAspProLysSerAsnLeuIleGln---TrpLeuSer 191
Db 559 ACGGTATGTCAACATGAGAACCCGGAAGGATCCCGGTCAAGCAGACTCTCTGTCT 618
QY 182 GlnGlnSerAspLeuGlyValIleSerLysThrPheGlnLeuSerSerHisProIleLeu 201
Db 619 TCTCAGAACCAAGCTTGGCGTCTTGGGACATTCCGGAACCTCGTCAACATG 678
QY 202 GlyAspTrpSerIleGlnValGlnValAsnAsp-----GlnThrTyrTyrGlnSer 218
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QY 219 PheGlnValSerGluTyrValLeuProLysPheGluValThrLeuGln-----ThrPro 236
Db 739 TTTGAGTGAAGAGTACGTCTGCGCCAGTTTCGAGTTCATAGTGAGCTACAGAGAA 798
QY 237 LeuTyrCysSerMetAsnSerLysHisLeuAsnGlyThrIleThrAlaLysTyrThr 256
Db 799 TTCTACTACATCTATACAGAGAGGCGCTGGAGTCCACCATCACCAGGTTCTCTAC 858
QY 257 GlyLysProValLysGlyAspValThrLeuThrPhe----- 268
Db 859 GGAAGAAAGTGGAGGAACCTGCTTGTCTTCGGATCCAGATGGCGAACAGAGG 918
QY 269 -----LeuProLeuSerPheTrpGlyLysLysLysAsn 279
Db 919 ATTTCCCTGCCTGAATCCCTCAAGCGCATTCGATTGAGGATGGCTCGGGGAGGTGTG 978
QY 280 IleThrLysThrPheLysIleAsnGlySerAlaAsnPheSerPheAsnAspGluGluMet 299
Db 979 CTGAGCCGGAAGTACTGCTGGACGGGGTGCAGAACCCCGACAGAACACCTGTGGGG 1038
QY 300 LysAsnValMetAspSerSerAsnGlyLeuSerGluTyrLeuAspLeuSerSerProGly 319
Db 1039 AGCTCTTGTACGTGCTGCC----- 1059
QY 320 ProValGluLeuLeuThrValThrGluSerValThrGlyIleSerArgAsnValSer 339
Db 1060 -----ACCGTCATCTTCACCTCAGGCGATGACATGTGTGACGAGAGCGC 1104
QY 340 ThrAsnValPhePheLysGlnHisAspTyrIleLeuPhePheAspTyrThrVal 359
Db 1105 AGCGGATCCCATCGTGACCTCTCCCTACAGATCCACTTCACCAAGACACCCCAAGTAC 1164
QY 360 LeuLysProSerLeuAsnPheThrAlaThrValLysValThrArgAlaAspGlyAsn--- 378
Db 1165 TTCAACACCAAGATGCCCTTTGACCTCATGTGTGTGTCAGCAACCTGTATGCTCTCCA 1224
QY 379 -----GlnLeuThrLeuGluArgArgAsnValValIleThrValThrGlnArg 396
Db 1225 GCCTACCGAGTCCCGTGGCAGTCCAGGGCGAGGACACTGTGAGTCTCTAACCCAGGGA 1284
QY 397 AsnTyrThrGluTyrTrpSerGlySerAsnSerGlyAsnGlnLysMetGluAlaValGln 416

Db 1285 GATGCGGTGGCCAAACTCAGCATCAACACACACCCCAAG----- 1329
QY 417 LysIleAsnTyrThrValProGlnSerGlyThrPheLysIleGluPheProIleLeuGlu 436
Db 1330 -----CCCTTGAGCATCATCGGTGCGCAGGAAGACAGAGCTCTCG 1371
QY 437 AspSerSerGluLeuGlnLeuLysAlaTyrPheLeuGlySerLysSerSerMetAlaVal 456
Db 1372 GAGGAGAGCAG-----GCTACGAGACCATGTCAGGCTCTG 1407
QY 457 HisSerLeuPheLysSerProSerLysThrTyrIleGlnLeuLysThr----- 472
Db 1408 CCTACAGCACCGTGGGCAACTCCAAATTAACCTGTCATCTCTCAGTCTAGTACAGAG 1467
QY 473 -----ArgAspGluAsnIleLysValGlySerProPheGluLeuValValSerGlyAsn 490
Db 1468 CTCAGACCCGGGAGACCCCTCAACGTCACTTCCTGCAATGAGACCGGCCACAG 1527
QY 491 LysArgLeuLysGluLeuSerTyrMetValValSerArgGlyGlnLeuValAlaValGly 510
Db 1528 GCCAAGATCCGCTACTACACTCTGATCATGAACAGGCGAGCTGTGAAGCGGGA 1587
QY 511 Lys-----GlnAsnSerThrMetPheSerLeuThrProGluAsnSer 524
Db 1588 CGCCAGTCCGAGACCCCGGCGAGACCTGGTGTGTGCTGCCCCCTGCTCCATCACCACCGAC 1647
QY 525 TrpThrProLysAlaCysValIleValTyrTyr-----IleGluAspAspGly 540
Db 1648 TTTCATCCCTTCCTTCGCTGTGTGCGTACTACGCTGATGCGTGCAGCGGCCAGAGG 1707
QY 541 GluIleIleSerAspValLeuLysIleProValGln-----LeuVal 554
Db 1708 GAGGTGTGGCGACTCCGTGTGGTGCAGCTCAAGGACTCTCTGCGTGGGTGCTGCTGTG 1767
QY 555 PheLysAsnLysIleLysLeuTyrTrpSerLysValLysAlaGlu----- 569
Db 1768 GTAAAAAGCGGC-----CAGTCAGAGACCGGCGAGCTGTA 1803
QY 570 ProSerGluLysValSerLeuArgIleSerValThrGlnProAspSerIleValGlyIle 589
Db 1804 CTGGGCGAGCAGATCACCTCGAATAGAGGTGACACCGGGCCCGGGTGTGTA---CTG 1860
QY 590 ValAlaValAspLysSerValAsnLeuMetAsnAlaSerAsnAspIleThrMetGluAsn 609
Db 1861 GTGGCGTGGACAGAGCGGTGTTCGTGCTGAATAAGAAACAACAACTGACACAGAGTAAG 1920
QY 610 ValValHisGluLeuGluLeuTyrAsnThrGlyTyrTyrLeuGlyMetPheMetAsnSer 629
Db 1921 ATCTGGGAGCTGGTGGAGAGGACAGCATCGCTGCACCCCGGCGAGTGGGAGGATTAC 1980
QY 630 PheAlaValPheGlnGluCysGlyLeuTrpValLeuThrAspAla----- 644
Db 1981 GCCGTGTCTTCTCCGACGCGAGGCTGACCTTCAGAGCAGCAGTGGCGCAGACCGCC 2040
QY 644 ----- 644
Db 2041 CAGAGGGCAGAACTTCAGTGCCCGCAGCGCCCGCCGAGCGCTTCGCTGTCAGCTC 2100
QY 645 -----AsnLeuThrLysAspTyrIle 651
Db 2101 ACGGAGAGCGAATGGACAAAGTCGGCAAGTACCCCAAGGAGCTGCGCAAGTGTGTCGAG 2160
QY 652 AspGlyValTyrAspAsn-----AlaGluTyrAlaGluArgPheMetGlu 666
Db 2161 GACGCGTGGGAGAACCCCATGAGGTTCCTGTCGCCAGCGCGGACCGCTTTCATCTCC 2220
QY 667 GluAsnGlu-----GlyHisIleValAspIleHis 676
Db 2221 CTGGCGAGGCGGTGCAAGAGGTCTTCTGAGTCTCTCAACTACATCAGAGGTGGGG 2280
QY 677 -----AspPheSerLeu 680
Db 677 ----- 680

Db 2281 CGGCAGCAGCGCGCGGCGCCAGCCACTGGCGCTGGCCAGGAGTAACCTGGATGAGGACATC 2340
Qy 681 GlySerProHisVal-----ArgLysHisPheProGluThrTrpLeu----- 696
Db 2341 ATTCAGAGAGAACATCGTTTCCGGAAGTAGGTTCCAGAGAGCTGGCTGTGGAGGTT 2400
Qy 697 -----LeuAspThrAsnMetGlyTyrArgIleTyr 706
Db 2401 GAGGACTTGAAGAGCCACCGAAATGGAATCTCTACGAAGCTC----- 2445
Qy 707 GlnGluPheGluValThrValProAspSerIleThrSerTrpValAlaThrGlyPheVal 726
Db 2446 -----ATGAATATATTTTGAAGACTCCATCACCAGTGGAGATCTTGGCTGTCCAGC 2499
Qy 727 IleSerGluAspLeuGlyLeuGlyLeuThrThrThrProValGluLeuGlnAlaPheGln 746
Db 2500 ATGTGGCAGAAAGGATC---TGTTGGCAGACCCCTTCGAGGTCCAGAGTAATGCAG 2556
Qy 747 ProPheIlePheLeuAsnLeuProTyrSerValIleArgGlyGluGluPheAlaLeu 766
Db 2557 GACTTCTTCATCGACCTCGCGCTACCTCTCTGTTCGAAACGAGCAGGTGGAAATC 2616
Qy 767 GluIleThrIlePheAsnTyrLeuLysAspAlaThrGluValLysValIleIleGlu--- 785
Db 2617 CGACCGCTTCTACAAATTAC---CGCAGAACCAAGAGCTCAAGGTGAGGTGGAACTA 2673
Qy 786 ---LysSerAspLysPheAspIleLeuMetThrSerSerGluIleAsnAlaThrGlyHis 804
Db 2674 CTCACAAATCCAGCTTCTCGAGCTGGCCACCAAGAGG-----CGTCAC 2721
Qy 805 GlnGlnThrLeuValProSerGluAspGlyAlaThrValLeuPheProIleArgPro 824
Db 2722 CAGCAGACCGTAACCATCCCGCCCAAGCTCTGTTGCTTCATATGTCATCGTGGCG 2781
Qy 825 -----ThrHisLeuGlyGluIleProIleThrValThrAlaLeuSerProThrAlaSer 842
Db 2782 CTAAAGACCGGCTGCAGGAAGTGAAGTCAAGCTGCCGTCTACCATCATTTTCATCAGT 2841
Qy 843 AspAlaValThrGlnMetIleLeuValLysAlaGluIleGlyLeuLysSerTyrSerGln 862
Db 2842 GACCGTGTGAGGAAGTCCCTGAAGGTCTGCCGGAAGGAATCAAGATGAACAAACTGTG 2901
Qy 863 SerIleLeuLeuAspLeuThrAspAsnArgLeu-----GlnSerThrLeuLysThrLeu 880
Db 2902 GCTGTT---CGCACCTGGATCCAGAACGCTCGGCGGTGAGAGTGCAGAAAGAG--- 2955
Qy 881 SerPheSerPheProAsnThrVal-----ThrGlySerGluArg 894
Db 2956 ---GACATCCACCTGCAGACCTCAGTGCAGCAAGTCCCGGACACCCGAGTCTGAGACC 3009
Qy 895 -----ValGlnIleThrAlaIleGlyAspValLeuGlyProSerIleAsnGly--- 910
Db 3010 AGAATTCCTCGAAGGAGCCCGGAGTGGCCAGATGACAGAGGATCGCTCGAGCGGAA 3069
Qy 911 ---LeuAlaSerLeuIleArgMetProTyrGlyCysGlyGluGlnAsnMetIleAsnPhe 929
Db 3070 CGGCTGAAGCACCTCAITGTGACCCCTCGGCTGCGGGACAGAACAGAACATGATCGGCATG 3129
Qy 930 AlaProAsnIleTyrIleLeuAspTyrLeuThrLysLysLysGlnLeuThrAspAsnLeu 949
Db 3130 ACGCCCAAGGTCATCGCTGTGCATTACTGATGAACCGGAGCAGTGGGAGAGTTCCGGC 3189
Qy 950 LysGluLys-----AlaLeuSerPheMetArgGlnGlyTyrGlnArgGluLeuLeu 966
Db 3190 CTAGAGAAGCGGAGCGGCGCTTGGAGCTCATCAAGAAGGGGTACACCCAGCAGCTGGCC 3249
Qy 967 TyrGlnArgGluAspGlySerPheSerAlaPheGlyAsnTyrAspProSerGlySerThr 986
Db 3250 TTCAGACACCCAGCTCTGCTGCTTGGCGCTTCGTGAAACCGGCACCC-----AGCACC 3303
Qy 987 TrpLeuSerAlaPheValLeuArgCysPheLeuGluAlaAspProTyrIleAspIleAsp 1006
Db 3304 TGGCTGACCGCTACGTGGTCAAGGCTCTTCTCTGCTCTCAACCTCATCGCCATCGAC 3363

Qy 1007 GlnAsnValLeuHisArgThrTyrThrTrpLeu---LysGlyHisGlnLysSerAsnGly 1025
Db 3364 TCCCAAGTCCCTCGCGGGCTGTTAAATGGCTGATCCTGGAGAAAGACAGACCGCGGG 3423
Qy 1026 GluPheTrpAspProGlyArgValIleHisSerGluLeuGlnGlyGly----- 1041
Db 3424 GTCCTCCAGGAGGATGCGCCCTGTATACACCAAGAAATGATGTGTGATACGGAACAAC 3483
Qy 1042 AsnLysSerProValThrLeuThrAlaTyrIleValThrSerLeuLeuGlyTyrArgLys 1061
Db 3484 AACGAGAAGACATGGCCCTCAGCGCTTGTCTCATCTCGCTG----- 3528
Qy 1062 TyrGlnProAsnIleAspVal---GlnGluSerIleHis----- 1073
Db 3529 ---CAGGAGGCTTAAGATATTTGCGAGGAGCAGGTCAACAGCCTGCCAGGCGCATCACT 3585
Qy 1074 -----PheLeuGluSerGluPheSerArgGlyIleSerAspAsnTyrThrLeu 1089
Db 3586 AAGCAGGAGACTTCTTGAAGCCCAACTAC---ATGAACCTACAGAGATCTCCTACTGTG 3642
Qy 1090 AlaLeuIleThrTyrAlaLeuSerSerValGlySerProLysAlaLysGluAlaLeuAsn 1109
Db 3643 GCATTTGCTGCTATGCTCTGCGCCAGATGGCAGGCTGAAGGGCGCTCTTCTTAACAAA 3702
Qy 1110 MetLeuThrTrpArgAlaGluGlnGlyMetGlnPheTrpValSerSerGluSer 1129
Db 3703 TTTCTGACC----- 3717
Qy 1130 LysLeuSerAspSerTrpGln-----ProArgSerLeuAspIleGluValAlaAla 1146
Db 3718 AAGATAGAACCCCTGGAGGACCTCGTAAGCAGCTCTACAAACGTGGAGGCCACATCC 3777
Qy 1147 TyrAlaLeuLeuSerHisPheLeuGlnPheGlnThrSerGluGlyIle---ProIleMet 1165
Db 3778 TATGCCCTCTTGGCC---CTACTGACGCTAAAAGACTTTTGACTTTGCTCCCTCGTGTG 3834
Qy 1166 ArgTrpLeuSerArgGlnArgAsnSerLeuGlyPheAlaSerThrGlnAspThrThr 1185
Db 3835 CGTTGGCTCANTGACAGAGATACTACGGTGTGGCTATGGCTCTACCCAGGCCACCTTC 3894
Qy 1186 ValAlaLeuLysAlaLeuSerGluPheAlaAla---LeuMetAsnThrGluArgThrAsn 1204
Db 3895 ATGGTGTTCGAAGCTTGGCTCAATACCAAAAGGACGCCCTGACCACAGAACTGAAC 3954
Qy 1205 IleGlnValThrValThrGlyProSerSer-----ProSerProLeu 1218
Db 3955 CTGTATGTCTCCCTCAACTGCCAGCGG-CAGCTCCAGATCACCCACCGTATCCACTG 4013
Qy 1219 AlaValValGlnProMetAlaVal-----Asn-IleSe 1229
Db 4014 GGAATCTCCAGCTCTCTCGATCAGAAGACCAAGAAATGAGGGTTTCACAGTCAC 4073
Qy 1229 -AlaAsnGlyPheGlyPheAlaIleCysGlnLeuAsnValValTyrAsnValLysAlaSe 1249
Db 4074 AGCTGAAGAAAGGCCCAAGGCACCTTCTCGTGGTGTGACAAATGTACCATGTAAAGCCAA 4133
Qy 1249 -xGlySerSerArgArgArgSerIleGlnAsnGlnAlaPheAspLeuAspValAl 1269
Db 4134 AGATCAACTCACCTGTAATAAA-----TTGACCTCAAGGTCAAC 4172
Qy 1269 aVal-----LysGluAsnLysAspAspLeuAsnHisValAspLe 1282
Db 4173 CATAAACCCAGCCCGGAAACAGAAAGAGCCCTCAGGATGCCAAGAACACATATGATCCT 4232
Qy 1282 uAsnValCysThrSerPheSerGlyProGlyArgSerGlyMetAlaLeuMetGluValAs 1302
Db 4233 TGAGATCTGTACAGGTACCGGGAGACCGAGATGCCACTATGTCTATATTTGGACATATC 4292
Qy 1302 mLeuLeuSerGlyPheMetValProSerGlu-----AlaIleSerLeuSe 1317
Db 4293 CATGATGATGGCTTGTCTCCAGACACAGATGACCTGAAGCAGCTGGCCAAATGTTGTGA 4352

QY 1317 rGluThrValIysLysValGluTyr-----AspHisGlyLysLeuAsnLe 1332
 Db 4353 CAGATACATCTCCAGTATGAGTGGACAAAGCCTTCCGATAGGAAACACCCCTCATCAT 4412
 QY 1332 uTyLeuAspSerValAsnGluThrGln---PheCysValAsnIleProAlaValargas 1351
 Db 4413 CTACCTGGACAAGGTCACACCTCTGAGGTAGTCTGCTAGCTTTCAAGTTCCACCAATA 4472
 QY 1351 nPheLysValSerAsnThrGlnAspAlaSerValSerIleValAspTyrTyrGluProAr 1371
 Db 4473 CTTTAAATGAGCTTATCCAGCCTGGAGCAGTCAAGGTCTACGCTATTACAACTGGA 4532
 QY 1371 gArgGlnAlaValArgSerTyrAsnSerGluVal-----LysLeuSerSerCysAs 1388
 Db 4533 GGAAGGTGACCGGTTCACCATCCGGAAGAGGAGTGAAGAGCTGAACAAG-----4587
 QY 1388 pLeuCysSerAspValGlnGlyCysArgProCysGluAsp 1401
 Db 4588 -CTCTGCGGTGAT--GAAGTGGCGCTGTGTGAGGAG 4623

RESULT 10

US-08-662-227-1
 ; Sequence 1, Application US/0866227
 ; Patent No. 5922320
 ; GENERAL INFORMATION:
 ; APPLICANT: VOGEL, CARL-WILHELM
 ; APPLICANT: BREDEHORST, REINHORST
 ; APPLICANT: KOCK, MICHAEL
 ; APPLICANT: FRITZINGER, DAVID
 ; TITLE OF INVENTION: RECOMBINANT PROCVF
 ; NUMBER OF SEQUENCES: 39
 ; CORRESPONDENCE ADDRESS:
 ; ADDRESSEE: OBLON, SPIVAK, MCLELLAND, MAIER & NEUSTADT,
 ; ADDRESSEE: P.C. JEFFERSON DAVIS HIGHWAY
 ; STREET: 1755 S. JEFFERSON DAVIS HIGHWAY
 ; CITY: ARLINGTON
 ; STATE: VA
 ; COUNTRY: USA
 ; ZIP: 22202

COMPUTER READABLE FORM:

; MEDIUM TYPE: Floppy disk
 ; COMPUTER: IBM PC compatible
 ; OPERATING SYSTEM: PC-DOS/MS-DOS
 ; SOFTWARE: Patent In Release #1.0, Version #1.30
 ; CURRENT APPLICATION DATA:
 ; APPLICATION NUMBER: US/08/662,227
 ; FILING DATE: 14-JUN-1996
 ; CLASSIFICATION: 530
 ; ATTORNEY/AGENT INFORMATION:
 ; NAME: OBLON, NORMAN F.
 ; REGISTRATION NUMBER: 24,618
 ; REFERENCE/DOCKET NUMBER: 1126-0107-0X
 ; TELECOMMUNICATION INFORMATION:
 ; TELEPHONE: 703-413-3000
 ; TELEFAX: 703-413-2220
 ; INFORMATION FOR SEQ ID NO: 1:
 ; SEQUENCE CHARACTERISTICS:
 ; LENGTH: 5948 base pairs
 ; TYPE: nucleic acid
 ; STRANDEDNESS: single
 ; TOPOLOGY: linear
 ; MOLECULE TYPE: cDNA
 ; US-08-662-227-1

Alignment Scores:

Pred. No.: 1.66e-85 Length: 5948
 Score: 894.00 Matches: 361
 Percent Similarity: 40.90% Conservative: 295
 Best Local Similarity: 22.51% Mismatches: 672
 Query Match: 12.17% Indels: 276
 DB: 2 Gaps: 56

US-10-020-095-4 (1-1428) x US-08-662-227-1 (1-5948)

QY 18 AlaAlaLeuAlaVal-----AlaProGlyProArgPheLeuValThrAla 32
 Db 31 GTGTCTTATTGATGGTGTTCCTCCAGGCTCTCTCATGGGCTCTCTACACCTCATCACC 90
 QY 33 ProGlyIleIleArgProGlyGlyAsnValThrIleGlyValGluLeuLeu---GluHis 51
 Db 91 CCGTCTGTGTTTCGGAACAGACACAGAGAGCAAAATTTTGGTGGAGGCCCATGGAGACAGT 150
 QY 52 CysProSerGlnValThrValIysAla-----GluLeuLeuIysAlaSer 67
 Db 151 ACTCCAAACACGCTTCACATCTTCTTCATGATTTTCACGGAACAGAAACCTTGTTC 210
 QY 68 AsnLeuThrValSerValLeuGluAlaGluGlyValPheGluLysGlySerPheLysThr 87
 Db 211 CAAACAGATAGATGATGAATCCAGCAGGAGCATGCTGTCACT-----CCAAC 261
 QY 88 LeuThrLeuProSerLeuProLeuAsnSerAlaAspGluIleTyrGluLeuArgValThr 107
 Db 262 ATAGAGATTCCAGCAAAAGAGTGGATGAGTACGCACTCCAGGCAAAATCAATATGTGGTGTG 321
 QY 108 GlyArgThrGlnAspGluIleLeuPheSerAsnSerThrArgLeuSerPheGluThrLys 127
 Db 322 CAAAGTAAGTGGTCTCCTCAAGTGAGATGGAAAAGGTGGTCTCTCTTCTTACCAGAGTAGC 381
 QY 128 ArgIleSerValPheIleGlnThrAspLysAlaLeuTyrLysProLysGlnGluValLys 147
 Db 382 -----TTTCTGTTTTATCCAGACAGATAAGGCATCTATACACACCGGTCTCCAGTACTC 435
 QY 148 PheArgIleValThrLeuPheSerAspPheLysProTyrLysThrSerLeuAsnIleLeu 167
 Db 436 TATCGTGTGTTTTCTATGGATCACAACAAGCAGAGATGAACAAACCTGATGTTGTGAG 495
 QY 168 IleLysAspProLysSerAsnLeuIleGlnThrLeuSerGlnGlnInSerAspLeuGly 187
 Db 496 TTTCAGACTCCAGAAGGCATTTCTGTCACT-----TCTAATTCAGTTGACCTAAAC 546
 QY 188 ValIleSerLysThrPheGlnLeuSerSerHisProIleLeuGlyAspTrpSerIle--- 206
 Db 547 TTCCTC---TGGCCTTACAATTTACCAGCCTGTGTAGTTGGGGACTTGGAGGATGTG 603
 QY 207 ---GlnValGlnValAsnAspGlnThrTyrTyrGlnSerPheGlnValSerGluTyrVal 225
 Db 604 GCCAAATATGAACATCCCCAGAGAAATATATCTCATATTTTGTATGTCAGGAAATATGTG 663
 QY 226 LeuProLysPheGluValThrLeuGlnThrPro-----LeuTyrCysSerMetAsn 242
 Db 664 TTGCCAAGCTTTGAAGTCCGCTCTCAACCATCAGAGAAGTTTTTTTATCATTCAGCGCAAT 723
 QY 243 SerLysHisLeuAsnGlyThrIleThrAlaLysTyrThrTyrGlyLysProValLysGly 262
 Db 724 ---GAAATTTCCAGGTGCTCATCTGCAAGGACTTGTATGAGGAGGAAGTGAAGGT 780
 QY 263 AspValThrLeuThrPheLeuProLeuSerPheTrpGlyLysLysAsnIle----- 280
 Db 781 ---GTGGCCTTTGTCTCTCTTGGAGTGAATAATAGATGATGCTAAAAAGAGATTCCAGAC 837
 QY 281 -----ThrLysThrPheLysIleAsnGlySerAlaAsnPheSerPheAsnAspGluGlu 298
 Db 838 TCATCAGAGAAATCCGATTATTGATGGAGATGGAAAGCAACACTAAAAAGAGATACA 897
 QY 299 MetLysAsnValMetAspSerSerAsnGlyLeuSerGluTyrLeuAspLeuSerSerPro 318
 Db 898 TTCGTTCTCGATTTCCAAATCTCAATGAGCTTGTGGGCATCTCTGTATGCATCT--- 954
 QY 319 GlyProValGluIleLeuThrValThrValThrGluSerValThrGlyIleSerArgAsnVal 338
 Db 955 -----GTAACAGTTCATCAGAGAAATCAGGCAGTGTATGTTAGTACTGAG 999
 QY 339 SerThrAsnValPhePheLysGlnHisAspTyrIleIleGluPhePheAspTyrThrThr 358
 Db 1000 CAAAGCGCATTCATATTTGGGCATCTCCCTATCAGATCCACTTCACAAAAACCCCAAA 1059

Db 3106 GGTATGCCAGCAGATGGTGTACAGAAAGCAGATCATCTTCATGACGACATTACAAAC 3165
QY 980 TyrAspProSerGlySerThrTrpLeuSerAlaPheValLeuArgCysPhe---LeuGlu 998
Db 3166 -----CGTCATCTAGTCTGGCTAACAGCATATGTGTAAAGTCTTTGCCATGGCT 3219
QY 999 AlaAspProTyrIleAspIleAspGlnAsnValLeuHisArgThrTyrThrTrpLeu--- 1017
Db 3220 GCCAAATAGTAGCAGCATATTAGTCATGAATCATTTGTGGAGGTGTGAGGTGGCTGATT 3279
QY 1018 LysGlyHisGlnLysSerAsnGlyGluPheTrpAspProGlyArgValIleHisSerGlu 1037
Db 3280 CTGAACAGGCAACACACAGATGAGCGGTTCAGAAATATGCCCTGTACTTCTCGAACA 3339
QY 1038 LeuGlnGly-----GlyAsnLysSerProValThrLeuThrAlaTyrIleValThr 1054
Db 3340 ATCAGGAGGAAATTCAGGTGTCTGAAGAGAGATATATTAAACAGCTTTCATTTCTGGTT 3399
QY 1055 SerLeuLeuGlyTyrArg-----LysTyrGlnProAsnIleAsp-----Val 1068
Db 3400 GCCTTTGTGAATCCAAACAATCTGCAATGACTATGTCAATAGTCTAGACAGCAGCATC 3459
QY 1069 GlnGluSerIlePheLeuGluSerGluPheSerArgGlyIleSerAspAsnTyrThr 1088
Db 3460 AAGAAGGCCCAAAATATTACTCAAAAAGTATGAGAAA---CTGCAAGGCCCTTACACT 3516
QY 1089 LeuAlaLeuIleThrTyrAlaLeuSerSerValGlySerProLysAlaLysGluAlaLeu 1108
Db 3517 ACAGCCCTCACAGCCCTATGCTTTGGCT-----GCTCAGACCAACATC 3558
QY 1109 AsnMetLeuThrTrpArgAlaGluGlnGluGlyMetGlnPheTrpValSerGlu 1128
Db 3559 AATGATCAGAGGTACTCATGGCAGCATCAACAGGAGGATCATTTGG----- 3606
QY 1129 SerLysLeuSerAspSerTrpGlnProArgSerLeuAspIleGluValAlaAlaTyrAla 1148
Db 3607 -----GAAGAATACATGTCTCACACCCACAACTTGAAGGCCACTTCTATGCTC 3654
QY 1149 LeuLeuSerHisPheLeuGlnPheGlnThrSerGluGlyIleProIleMetArgTrpLeu 1168
Db 3655 TTGTTGGCCCTGTGAAATGAAGAATTTGATCAAACTGGTCCCATAGTCAGATGGCTG 3714
QY 1169 SerArgGlnArgAsnSerLeuGlyGlyPheAlaSerThrGlnAspThrThrValAlaLeu 1188
Db 3715 ACAGATCAGAAATTTTATGGGAAACATATATGGCAAAACCAACACAGTATGGCATTT 3774
QY 1189 LysAlaLeuSerGluPheAlaAlaLeuMetAsnThrGluArg---ThrAsnIleGlnVal 1207
Db 3775 CAAGCTCTGTGTAATAGATTCAGATGCCTACCCATAAGAGACTTAAACTTAGATATT 3834
QY 1208 ThrValThrGlyProSerSerProSerProLeu----- 1218
Db 3835 ACTATTGAAGTCCGATCGAGNAGTACCTATAGGTACAGATTAATTAATAAATGCT 3894
QY 1219 -----AlaValValGlnPro-----MetAlaValAsnIleSerAlaAsnGly 1232
Db 3895 CTCCTGGCTCGGACAGTAGAGACCAAACTCAACCAAGACATCACGTGACAGCATCAGT 3954
QY 1233 PheGlyPheAlaIleCysGlnLeuAsnValValTyrAsnValLysAlaSerGlySerSer 1252
Db 3955 GATGGAAGACCAATAGACCATTTTGGACATTTCTATAACGCACAGTTG----- 4002
QY 1253 ArgArgArgSerIleGlnAsnGlnGluAlaPheAspLeuAspValAlaValLysGlu 1272
Db 4003 CAGGAGAAGGCAATGTTTGCATAAA-----TTTCATCTTAATGTTCTCTGTGAA--- 4053
QY 1273 AsnLysAspAspLeuAsnHisValAsp-----LeuAsnValCysThr 1286
Db 4054 ---AACATCCACTTGAATCAATGGAGGCAAGGAGCCCTCATGCTCAAGATCTGCACA 4110
QY 1287 SerPheSerGlyProGlyArgSerGlyMetAlaLeuMetGluValAsnLeuSerGly 1306
Db 4111 AGGTATCTGGAGAACTTGTATCTCAATGACATTAATTTCTATGCTGCTGCT 4170

QY 1307 PheMetValProSerGluAlaIleSer-----LeuSerGluThrValLys 1321
Db 4171 TTTCCTCCCTGATGCTGAGAGACCTTACAGGCTTCTAAGAGGTGACAGATACATCTCC 4230
QY 1322 LysValGluTyrAspHisGlyLysLeuAsn-----LeuTyrIleuAspSer 1336
Db 4231 AGATATGAAGTGTGACAATAATATGCTCAGAAAGTAGCTGTATCATTTACTTAAACAAG 4290
QY 1337 ValAsnGluThrGln---PheCysValAsnIleProAlaValArgAsnPhelLysValSer 1355
Db 4291 GTCTCCCACTCTGAAGATGAATGCTGCACCTTAAAGATTCACAGCATTTTGAAGTTGGC 4350
QY 1356 AsnThrGlnAspAlaSerValSerIleValAspTyrTyrGluProArgGlnAlaVal 1375
Db 4351 TTCAATTCAGCCAGGATCAGTCAAGGTGTACAGCTACTACAATCTAGATGAAATAATGTACC 4410
QY 1376 ArgSerTyrAsnSerGluValLysLeuSerSerCysAspLeuCysSerAspValGlnGly 1395
Db 4411 AAGTTCTACCATCCAGATAAAGAACAGGCTTCTCAATAAGATATGATTGGTAACGTT 4470
QY 1396 CysArgProCysGluAspGlyAlaSerGlySerHisHis----- 1408
Db 4471 TGCCGATGTGCAGGAGAAACCTGTTCTCGCTCAACCATCAGGAAAGGATTTGATGTTCCA 4530
QY 1409 -----HisSerSerValIlePheIlePheCysPheLysLeuLeu 1421
Db 4531 TTACAAATTGAAAGCCTCGCAGACGAATGTGGATTATGTCTACAAACCAAGCTGCTT 4590
QY 1422 TyrPheMetGlu 1425
Db 4591 CGAATAGAGAA 4602

RESULT 11

US-09-017-947-1
; Sequence 1, Application US/09017947
; Patent No. 6303754
; GENERAL INFORMATION:
; APPLICANT: VOGEL, CARL-WILHELM
; APPLICANT: BREDEHORST, REINHORST
; APPLICANT: KOCK, MICHAEL
; APPLICANT: FRITZINGER, DAVID
; TITLE OF INVENTION: RECOMBINANT PROCVF
; NUMBER OF SEQUENCES: 39
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: OBLON, SPIVAK, MCCLELLAND, MAIER & NEUSTADT,
; ADDRESSEE: P.C.
; STREET: 1755 S. JEFFERSON DAVIS HIGHWAY
; CITY: ARLINGTON
; STATE: VA
; COUNTRY: USA
; ZIP: 22202
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/017,947
; FILING DATE:
; CLASSIFICATION:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/662,227
; FILING DATE: 14-JUN-1996
; ATTORNEY/AGENT INFORMATION:
; NAME: OBLON, NORMAN F.
; REGISTRATION NUMBER: 24,618
; REFERENCE/POCKET NUMBER: 1126-0107-0X
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 703-413-3000
; TELEFAX: 703-413-2220
; INFORMATION FOR SEQ ID NO: 1:
; SEQUENCE CHARACTERISTICS:

; LENGTH: 5948 base pairs
 ; TYPE: nucleic acid
 ; STRANDEDNESS: single
 ; TOPOLOGY: linear
 ; MOLECULE TYPE: cDNA
 US-09-017-947-1

Alignment Scores:

Pred. No.: 1.66e-85 Length: 5948
 Score: 894.00 Matches: 361
 Percent Similarity: 40.90% Conservative: 295
 Best Local Similarity: 22.51% Mismatches: 672
 Query Match: 12.17% Indels: 276
 DB: 4 Gaps: 56

US-10-020-095-4 (1-1428) x US-09-017-947-1 (1-5948)

QY	18	AlaAlaLeuAlaVal-----AlaProGlyProArgPheLeuValThrAla	32
DB	31	GCTGCTCTATTGATGGTTTCCAGGGCTCTCTCATGGGGCTCTCTACACCCCTCATCAC	90
QY	33	ProGlylleleArgProGlyGlyAsnValThrIleGlyValGluLeuLeu---GluHis	51
DB	91	CCTGCTGTTTGGCAACAGACACAGAGACCAAAATTTTGGTGGAGCCCATGGAGACAGT	150
QY	52	CysProSerGlnValThrValLysAla-----GluLeuLeuLysThrAlaSer	67
DB	151	ACTCCAAAACAGCTTGACATCTTGTTCATGATTTTCCAGGAAGCAGAAAACCTTGTTC	210
QY	68	AsnLeuThrValSerValLeuGluAlaGluGlyValPheGluLysGlySerPheLysThr	87
DB	211	CAAAACAGAGTAGATATGAATCCAGCAGGAGGAGCTGCTGCTCACT-----CCAACT	261
QY	88	LeuThrLeuProSerLeuProLeuAsnSerAlaAspGluIleTyrgluLeuArgValThr	107
DB	262	ATAGAGATTCAGAAAAGAGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG	321
QY	108	GlyArgThrGlnAspGluIleLeuPheSerAsnSerThrArgLeuSerPheGluThrLys	127
DB	322	CAAGTAACGTCTCTCAAGTGAGATTGGAAAAGGTGGTCTCTCTTCTTACCAAGATAGC	381
QY	128	ArgIleSerValPheIleGlnThrAspLysAlaLeuTyrlsProLysGlnGluValLys	147
DB	382	-----TTTCTGTTTATCCAGACAGATAAGGAGGAGGAGGAGGAGGAGGAGGAGGAG	435
QY	148	PheArgIleValThrLeuPheSerAspPheLysProTyrlsThrSerLeuAsnIleLeu	167
DB	436	TATCGTCTTTTCTATGGATCAACACACAGCAAGATGAACAAACTGTGTGTGTAG	495
QY	168	IleLysAspProLysSerAsnLeuIleGlnThrLysSerGlnGlnSerGlnSerAspLeuGly	187
DB	496	TTTCAGACTCCAGAAAGGCATTTCTGTGAGT-----TCTAATTCAGTTGACCTAAAC	546
QY	188	ValIleSerLysThrPheGlnLeuSerSerHisProIleLeuGlyAspTrpSerIle---	206
DB	547	TTCTTCTC---TGGCCTTACATTTACCAACCTGTCTAGTTGGGAGCTTGGAGATTGTG	603
QY	207	---GlnValGlnValAsnAspGlnThrTyrlsGlnSerPheGlnValSerGluTyrlsVal	225
DB	604	GCCAAATATGAACATCCCAAGAGATATATATATATATATATATATATATATATATATAT	663
QY	226	LeuProLysPheGluValThrLeuGlnThrPro-----LeuTyrlsCysSerMetAsn	242
DB	664	TTGCCAAGCTTTGAAGTCGCTGCCAACCATCAGAGAGGTTTTTTTACATTCAGCGCAAT	723
QY	243	SerLysHisLeuAsnGlyThrIleThrAlaLysTyrlsThrTyrlsGlyLysProValLysGly	262
DB	724	---GAAAATTTCCACGCTCTCTACTGCAAGGAGTACTTGTATGAGAGGAGGAGGAGGAG	780
QY	263	AspValThrLeuThrPheLeuProLeuSerPheTrpGlyLysLysLysAsnIle-----	280
DB	781	---GTGGCCCTTTGTCCTTTTGGAGTGAAAATAGATGATGCTAAAAGAGATTTCAGAC	837
QY	281	-----ThrLysThrPheLysIleAsnGlySerAlaAsnPheSerPheAsnAspGluGlu	298
DB	838	TCACTCAGAGAAATTCGATTAATGATGGAGATGGGAAACCAACACTAAAAAGAGATACA	897
QY	299	MetLysAsnValMetAspSerSerAsnGlyLeuSerGluTyrlsLeuAspLeuSerSerPro	318
DB	898	TTCCGTTCTCGAATTCCAAAATCTCAATGAGCTTGTGGGCATCTCTGTATGATCATCT---	954
QY	319	GlyProValGluIleLeuThrValThrGluSerValThrGlyIleSerArgAsnVal	338
DB	955	-----GTAACAGCTCATCAGCAATCAGCAGTGTATGATGAGTGTAGTACTGAG	999
QY	339	SerThrAsnValPhePheLysGlnHisAspTyrlleIleGluPhePheAspTyrlsThr	358
DB	1000	CAAGCGGCAATTCATATTGTGGCATCTCCCTATCAGATCCACTTCACAAAAACCCCAAA	1059
QY	359	ValLeuLysProSerLeuAsnPheThrAlaThrValLysValThrArgAlaAspGlyAsn	378
DB	1060	TATTTCAAGCCAGGAATGCCATATGAACCTGAGTGTATGTTACCAACCTGTATGGCTCA	1119
QY	379	GlnLeuThrLeuGluGluArgAsnValValIleThrValThrGlnArgAsnTyrls	398
DB	1120	CCAGCT-----GCCCATCTGCCAGTGGTATCAGAGGCCCTTT	1155
QY	399	ThrGluTyrlsSerGlySerAsnSerGlyAsnGlnLysMetGluAlaValGlnLysIle	418
DB	1156	-----CATTTCTATGGAAACCACTTTGAGTGTAGTGGAGCTGTAAAGCTC	1197
QY	419	AsnTyrlsThrValProGlnSerGlyThrPheLysIleGluPheProIleLeuGluAspSer	438
DB	1198	ATCTCGAATACATCAATGAACTGCTCA-----AGCTTACCAATCACTGTGTAGAACT	1248
QY	439	SerGluLeuGlnLeuLysAlaTyrlsPheLeuGlySerLysSerMetAlaValHisSer	458
DB	1249	AACCATGAGACCTCCCAAGAAACCGCAGGCAACAAAGTCCATGACGACCATACCTAC	1308
QY	459	LeuPheLysSerProSerLysThrTyrlleGlnLeuLysThrArgAspGluAsnIleLys	478
DB	1309	CAACCCAGGAGAGATCTGAAACTATCTTCATCTAGCATTACATCTACAGAGATTAG	1368
QY	479	ValGlySer-----ProPheGluLeuValSerGlyAsn-----LysArg	492
DB	1369	CCCGAGATAACTTACCTGTCAATTCATGTAAGGCAATGCAAAATTCCTGTAAGCAG	1428
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QY	512	-----GlnAsnSerThrMetPheSerLeuThrProGluAsnSerTrpThr	526
DB	1489	CCAGGAGATGGGAGAACTCTGGTGCATGATGATGATGATGATGATGATGATGATGATGAT	1548
QY	527	ProLysAlaCysValIleValTyrlleGluAspAspGlyGluIleIleSerAspVal	546
DB	1549	CTTCTCTTCCGGTTGTGGCTTACTTACCAAGTGGGAAACCAACGAAATTTGGCTGATCT	1608
QY	547	LeuLysIleProValGln-----LeuValPheLys-----AsnLys	558
DB	1609	GTCTGGGTGGATGTGAAGATACCTGCAATGGGAGCTGTGTGTGAAAGGAGACAACTA	1668
QY	559	IleLysLeuTyrlsTrpSerLysValLysAlaGluProSerGluLysValSerLeuArgIle	578
DB	1669	ATACAAATG-----CCAGGAGCTGCAATGAAATCAAAATG	1704
QY	579	SerValThrGlnProAspSerIleValGlyIleValAlaValAspLysSerValAsnLeu	598
DB	1705	GAA-----GGGGATCCAGGTCTCGGGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGT	1761
QY	599	MetAsnAlaSerAsnAspIleThrMetGluAsnValValHisGluLeuLeuTyrlsAsn	618
DB	1762	CTCAATGATAAATAAAGATTAGCAAGCTAAGATATGGGACACAAATAGAAAGAGTGAC	1821
QY	619	ThrGlyTyrlsTyrlsLeuGlyMetPheMetAsnSerPheAlaValPheGlnGlyCysGlyLeu	638

Db 1822 TTTGGCTGTACAGTGGCAGTGGCCAGATAATCTGGGTGTGTTGAGAGTGTGGACTG 1881
QY 639 TrpValLeuThrAspAlaAsnLeu-----ThrLysAsp----- 649
Db 1882 GCTCTGACCAACAGCACTAATCTCAACACCACAGAGATCAGCTGCAAAAGTCTCTCAG 1941
QY 649 ----- 649
Db 1942 CTTGCAANTCGAGGGCTGCCAGTCTCTGTGTTTCTGCTTGACAGCAACGCAAGCAAGCG 2001
QY 649 ----- 649
Db 2002 GCAGAAATTTCCAGGATCAAGACCTGCGTAATGCTGTGAAGATGTCATGATGAGAACCC 2061
QY 649 ----- 649
Db 2062 ATGGGGTACCTTGTAAGAGCTGCAAAATACATCCAGAGGGAGATGCTGTGAAGCT 2121
QY 650 -----TyrIleAspGlyValTyAsp---AsnAlaGluTyAla 661
Db 2122 GCCTTCTTGAATGCTGCTGCTACATCAAGGGGTCGAGATGAARACCAACCGGAGAGC 2181
QY 662 GluArgPheMet-----GluGluAsnGlu---GlyHisIleValAspIleHisaspPhe 678
Db 2182 GAGTTGTTCTGCAAGAGATGATAATGAAGATGGTTTCATAGCATAGTATCATC 2241
QY 679 SerLeuGlySerProHisValArgLysHisPheProGluThrTrpIleLeu--- 697
Db 2242 TCA-----AGTCTGATTCCCAAGTTGGTGGCTGAACA 2280
QY 698 -----AspThrAsnMetGlyTyArgIleTyGlnGluPheGluValThr 712
Db 2281 AAGGACTTGACCGAGGAGCTTAACAGTCAAGGGATTTCGAAGCAAGACAAATGCTTTTAT 2340
QY 713 ValProAspSerIleThrSerTrpValAlaThrGlyPheValIleSerGluAspLeuGly 732
Db 2341 CTGAGGATTCATCAACACCTGGTGGTGGCTGTAAGCTTACACCCACCAAGGG 2400
QY 733 LeuGlyLeuThrThrProValGluLeuGlnAlaPheGlnProPheIlePheLeu 752
Db 2401 ATC---TGTGTGGCTGAACCTTATGAATAAGAGTCATCAAGAGCTTCTTCATGATCTT 2457
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Db 2458 CAAATCCCATATTCAGTAGTGAAGATGACGAGGTGGAGATTCGAGCTATTCTGCACAA 2517
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QY 813 GluAspGlyAlaThrValLeuPheProIleArgProThrHisLeuGly-----GluIle 830
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Db 2746 GTTGTACCTGAAGGGGTACAGAAATCCATTGTGACTATTGTTAAACTGGACCCCAAGGCA 2805
QY 871 AsnArgLeuGlnSerThr-----LeuLysThrLeuSerPhePhe 884
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QY 885 ProProAsnThrValThrGlySerGluArgValGlnIleThrAlaIleGlyAspValLeu 904
Db -----

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QY 905 GlyProSerIleAsnGly-----LeuAlaSerLeuIleArgMetProTyArgCysGly 922
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Db 2986 GAGCAAAATATGATCCGATGCGCCGACCACTATTATGCCACTACTACTCGACACCA 3045
QY 940 ThrLysLysLysGlnLeuThrAspAsnLeuLysGluLysAlaLeuSerPheMetArgGln 959
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QY 960 GlyTyArgGluLeuLeuTyArgGlnArgGluAspGlySerPheSerAlaPheGlyAsn 979
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QY 999 AlaAspProTyIleAspIleAspIleAsnValLeuHisArgThrTyThrTrpLeu--- 1017
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QY 1018 LysGlyHisGlnLysSerAsnGlyGluPheTrpAspProGlyArgValIleHisSerGlu 1037
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QY 1069 GlnGluSerIleHisPheLeuGluSerGluPheSerArgGlyIleSerAspAsnTyThr 1088
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QY 1089 LeuAlaLeuIleThrTyAlaLeuSerSerValGlySerProLysAlaLysGluAlaLeu 1108
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QY 1149 LeuLeuSerHisPheLeuGlnPheGlnThrSerGluGlyIleProIleMetArgTrpLeu 1168
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QY 1189 LysAlaLeuSerGluPheAlaLeuMetAsnThrGluArg---ThrAsnIleGlnVal 1207
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QY 1208 ThrValThrGlyProSerSerProSerProLeu----- 1218
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Db 4003 CAGGAGAAGCAAAATGTTTGCATAAA-----TTTCATCTTAATGTTTCTCTTGAA---4053
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QY 1287 SerPheSerGlyProGlyArgSerGlyMetAlaLeuMetGluValAsnLeuLeuSerGly 1306
Db 4111 AGGTATCTGGGAGAAGTTGATCTACAATGACAATAATTGATATTTCTATGCTGACTGT 4170
QY 1307 PheMetValProSerGluAlaIleSer-----LeuSerGluThrValLys 1321
Db 4171 TTTCTCCTCCTGATCTGAAGACCTTACAAGCCTTTTAAAGAGTGGACAGATACATCTCC 4230
QY 1322 LysValGluTyrAspHisGlyLysLeuAsn-----LeuTyrLeuAspSer 1336
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QY 1337 ValAsnGluThrGln---PheCysValAsnIleProAlaValArgAsnPhelValSer 1355
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Db 4471 TGCGATGTGCAGAGAAACCTGTTCTCCTCACCATCAGGAAGAGTATGATGTTCACA 4530
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RESULT 12

US-09-925-442-1

; Sequence 1, Application US/09925442

; Patent No. 6607897

; GENERAL INFORMATION:

; APPLICANT: VOGEL, CARL-WILHELM

; BREDEHORST, REINHORST

; KOCK, MICHAEL

; FRITZINGER, DAVID

; TITLE OF INVENTION: RECOMBINANT PROCVF

; NUMBER OF SEQUENCES: 39

; CORRESPONDENCE ADDRESS:

; ADDRESSEE: OBLON, SPIVAK, MCCLELLAND, MAIER & NEUSTADT,

; P.C.

; STREET: 1755 S. JEFFERSON DAVIS HIGHWAY

; CITY: ARLINGTON

; STATE: VA

; COUNTRY: USA

; ZIP: 22202

; COMPUTER READABLE FORM:

; MEDIUM TYPE: Floppy disk

; COMPUTER: IBM PC compatible

; OPERATING SYSTEM: PC-DOS/MS-DOS

; SOFTWARE: Patentin Release #1.0, Version #1.30

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; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/925,442
; FILING DATE: 10-Aug-2001
; CLASSIFICATION: <Unknown>
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 09/017,947
; FILING DATE: <Unknown>
; ATTORNEY/AGENT INFORMATION:
; NAME: OBLON, NORMAN F.
; REGISTRATION NUMBER: 24,618
; REFERENCE/DOCKET NUMBER: 1126-0107-0X
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 703-413-3000
; TELEFAX: 703-413-2220
; INFORMATION FOR SEQ ID NO: 1:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 5948 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: cDNA
; SEQUENCE DESCRIPTION: SEQ ID NO: 1:
US-09-925-442-1
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Alignment Scores:

Pred. No.:	1,66e-85	Length:	5948
Scores:	894.00	Matches:	361
Percent Similarity:	40.90%	Conservative:	295
Best Local Similarity:	22.51%	Mismatches:	672
Query Match:	12.17%	Indels:	276
DB:	4	Gaps:	56

US-10-020-095-4 (1-1428) x US-09-925-442-1 (1-5948)

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QY 33 ProGlyIleIleAlaArgProGlyGlyAsnValThrIleGlyValGluLeuLeu---GluHis 51
Db 91 CTTGCTGTTTGGCAACAGACAGACAGAGAGCAAAATTTGTGGAGGCCCATGGAGACAGT 150
QY 52 CysProSerGlnValThrValLysAla-----GluLeuLeuLysThrAlaSer 67
Db 151 ACTCCAAACACAGCTTGACATCTTTGTTTCATGATTTTCCACGGAAGCAGAAACCTTGTTC 210
QY 68 AsnLeuThrValSerValLeuGluAlaGluGlyValPheGluLysGlySerPheLysThr 87
Db 211 CAACACGAGTAGATATGATCCAGCAGGAGGCATGCTGTCTACT-----CCAACT 261
QY 88 LeuThrLeuProSerLeuProLeuAsnSerAlaAspGluIleTyrGluLeuArgValThr 107
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QY 128 ArgIleSerValPheIleGlnThrAspLysAlaLeuTyrLysProLysGlnGluValLys 147
Db 382 -----TTTCTGTTTATCCACAGATAAAGGCATCTATACACGAGGTCTCCAGTACTC 435
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Db	664	TTGCCAAGCTTTGAAGTCGCTGCACCATCAGAGAAGTTTITTTACATTGACGGCAAT	723
Qy	243	SerLysHisLeuAsnGlyThrIleThrAlaLysTyrThrTyrGlyLysProValLysGly	262
Db	724	---GAAATTTCCACGCTGCTCATCAGTCAAGGTAAGTCTGTATGAGAGGAAGTGAAGGT	780
Qy	263	AspValThrLeuThrPheLeuProLeuSerPheTrpGlyLysLysLysAsnIle-----	280
Db	781	---GTGGCCTTTGTCTCTTTGGAGTGAATAAGATAGATGCTATAAAGAGTATTTCCAGAC	837
Qy	281	-----ThrLysThrPheLysIleAsnGlySerLalaAsnPheSerPheAsnAspGlu	298
Db	838	TCATCTCAGAGAATTTCCGATTATTTGATGGAGATGGAAAGCAACACTAAAAAGAGATACA	897
Qy	299	MetLysAsnValMetAspSerSerAsnGlyLeuSerGluTyrLeuAspLeuSerSerPro	318
Db	898	TTCCGTTCTCGATTTCCAAATCTCAATGAGCTTCTTGGCATACTCTGTATGATCT---	954
Qy	319	GlyProValGluIleLeuThrThrValThrGluSerValThrGlyIleSerArgAsnVal	338
Db	955	-----GTAACAGTCAACAGAAATCAGGCAGTATATGTTAGTACTGACTGAG	999
Qy	339	SerThrAsnValPhePheLysGlnHisAspTyrIleIleGluPhePheAspTyrThrThr	358
Db	1000	CAAAAGCGCATTCATATTTGGCATCTCCCTATCAGATTCACATTCACAAAACCCCCAAA	1059
Qy	359	ValLeuLysProSerLeuAsnPheThrAlaThrValLysValThrArgAlaAspGlyAsn	378
Db	1060	TATTTCAAGCGAGAATGCCATATGAATCAACGCTGTATGTTACCAACCTGATGGTCA	1119
Qy	379	GlnLeuThrLeuGluGluArgArgAsnAsnValValIleThrValThrGlnArgAsnTyr	398
Db	1120	CCAGCT-----GCCCATGTGCGAGTGGTATCAGAGGCCCTTT	1155
Qy	399	ThrGluTyrTrpSerGlySerAsnSerGlyAsnGlnLysMetGluAlaValGlnLysIle	418
Db	1156	-----CATTCATGGGAACCATTTTGATGATGGAGCTGTCTAAGCTC	1197
Qy	419	AsnTyrThrValProGlnSerGlyThrPheLysIleGluPheProIleLeuGluAspSer	438
Db	1198	ATCCGTAACATACCATTGAATGCTCAA-----AGCCTACCAATCATCTGTAGAACT	1248
Qy	439	SerGluLeuGlnLeuLysAlaTyrPheLeuGlySerLysSerSerMetAlaValHisSer	458
Db	1249	AACCATGGAGACCTCCCAAGAGAACGCCAGCAAAAGTCCATGACAGCCATAGCCCTAC	1308
Qy	459	LeuPheLysSerProSerLysThrTyrIleGlnLeuLysThrArgAspGluAsnIleLys	478
Db	1309	CAAAACCGAGGAGGATCTGAAACTATCTTCATGTAGCCATTACATCTACAGAGATTAA	1368
Qy	479	ValGlySer-----ProPheGluLeuValValSerGlyAsn-----LysArg	492
Db	1369	CCCGGAGATAACTTACCTGTCAATTTCAATGTGAAGGCGCAATGCAATTCACATGACGAC	1428
Qy	493	LeuLysGluLeuSerTyrMetValLysSerArgGlyGlnLeuValAlaValGlyLys---	511
Db	1429	ATCAAAATATTTCATACACTCATATTGAATAAAGGGAAGATTTTCAAGGTTGCGAGCAA	1488
Qy	512	-----GlnAsnSerThrMetPheSerLeuThrProGluAsnSerTyrThr	526
Db	1489	CCCAGGAGAGATGGCGAAGATCTGGTGACCATGATCTGATATCATCTCAGATCTCATC	1548
Qy	527	ProLysAlaCysValIleValTyrTyrIleGluAspAspGlyGluIleIleSerAspVal	546
Db	1549	CCTTCTTCGGTTTGTGGCTTACTCAAGTGGGAAACCAACCAATTTGGGTGATCT	1608

Qy	547	LeuLysIleProValGln-----LeuValPheLys-----AsnLys	558
Db	1609	GTCCTGGGTGGATGTGAAGGATACCTGCATCGGAACGTTGGTTGTGAAAGAGAGACAATCTA	1668
Qy	559	IleLysLeuTyrTrpSerLysValLysAlaGluProSerCluLysValSerLeuArgIle	578
Db	1669	ATACAAATG-----CCAGGAGCTCCAATGAAATCAAAATG	1704
Qy	579	SerValThrGlnProAspSerIleValGlyIleValAlaValAspLysSerValAsnLeu	598
Db	1705	GAA---GGGGATCCAGGTGCTCGGGTGGTCTTGTGGTGTGACAAAGCAGTATATGTT	1761
Qy	599	MetAsnAlaSerAsnAspIleThrMetGluAsnValValHISgluLeuGluLeuTyrAsn	618
Db	1762	CTCAATGATAAATATAGATATAGCCAGCTAAGATATGGGACACAATAGAAAGAGATGC	1821
Qy	619	ThrGlyTyrTyrLeuGlyMetPheMetAsnSerPheAlaValPheGlnGluCysGlyLeu	638
Db	1822	TTTGGCTGTACAGCTGGCAGTGGCCAGATAATCTGGGTGTGTTTCAAGATGCTGGACTG	188
Qy	639	TrpValLeuThrAspAlaAsnLeu---ThrLysAsp-----	649
Db	1882	GCTCTGACACCCAGCACTAATCTCAACACCAACAGAGATCAGCTGCAAAAGTGTCTCTCAG	1941
Qy	649	-----	649
Db	1942	CCTGCAATCGGAGCGTCCAGTCTGTGTTTCTGCTTCACAGCAACCAACGAAGCG	2001
Qy	649	-----	649
Db	2002	GCAGAAATTCAGGATCAAGACCTCGCTAAATGCTGTGAAGATGTCATGTCATGAGAACCC	2061
Qy	649	-----	649
Db	2062	ATGGGTACACTTGTGAAAGCGTGCAAAATACATCCAGGAGGAGATGCTGTGAAGCT	2121
Qy	650	-----TyrIleAspGlyValTyrAsp---AsnAlaGluTyrAla	661
Db	2122	GCCTTCTTGAATGCTGCTCATACATCAAGGGGCTCCGAGATGCAAAACCAACGGGAGAGC	2181
Qy	662	GluArgPheMet-----GluGluAsnGlu---GlyHisIleValAspIleHisAspPhe	678
Db	2182	GAGTTGTTCTGCAGAGAGATGATAAGAAGTGGTTTCATGACGATAGTATGATCATC	2241
Qy	679	SerLeuGlySerSerProHisValArgLysHisPheProGluThrTrpIleTrpLeu---	697
Db	2242	TCA-----AGGTCTGATTTCCCAAGAGTGGTGTGGCTAACCA	2280
Qy	698	-----AspThrAsnMetGlyTyrArgIleTyrGlnGluPheGluValThr	712
Db	2281	AAGGACTTGACGAGGAGCTAACAGCTCAAGGGAATTCAGCAAGACATGCTCTTTTAT	2340
Qy	713	ValProAspSerIleThrSerTrpValAlaThrGlyPheValIleSerGluAspLeuGly	732
Db	2341	CTGAGGATTCATACACCTGGTGGTGGTGTGAAGCTTTACACCCACCAAGGG	2400
Qy	733	LeuGlyLeuThrThrThrProValGluLeuGlnAlaPheGlnProPhePheIlePheLeu	752
Db	2401	ATC---TGTTGCTGAACTTATGAAATAAGAGTCATGAAAGTCTTCTTCATGATCTT	2457
Qy	753	AsnLeuProTyrSerValIleArgGlyGluGluPheAlaLeuGluIleThrIlePheAsn	772
Db	2458	CAATGCCATATTCAGTAGTAGAATGACGAGGTGGAGATTCGAGCTATTCTGCACACAC	2517
Qy	773	TyrLeuLysAspAlaThrGluValLysValIleIleGluLysSerAspLysPheAspIle	792
Db	2518	TACGTTAACGAGGATATTATGTGCGAGTGGAACTGTTATACAAACCCAGCCCTTC	2571
Qy	793	LeuMetThrSerSerGluIleAsnAlaThrGlyHisGlnGlnThrLeuLeuValProSer	812
Db	2572	-----TGCAATGCTTCCAAAAGGACAAAGACCCGACAGCTGCCAATTAAGCC	2625
Qy	813	GluAspGlyAlaThrValLeuPheProIleArgProThrHisLeuGly-----GluIle	830

APPLICANT: VOGEL, CARL-WILHELM
 TITLE OF INVENTION: DNA ENCODING COBRA C3, CVF1, AND CVF2
 NUMBER OF SEQUENCES: 81
 CORRESPONDENCE ADDRESS:
 ADDRESSEE: OBLON, SPIVAK, MCLELLAND, MAIER & NEUSTADT,
 ADDRESS: P.C. Jefferson Davis Highway, Suite 400
 STREET: 1755 S. Arlington
 CITY: Arlington
 STATE: Virginia
 COUNTRY: U.S.A.
 ZIP: 22202
 COMPUTER READABLE FORM:
 MEDIUM TYPE: Floppy disk
 COMPUTER: IBM PC compatible
 OPERATING SYSTEM: PC-DOS/MS-DOS
 SOFTWARE: Patent In Release #1.0, Version #1.25
 CURRENT APPLICATION DATA:
 APPLICATION NUMBER: US/08/447,411
 FILING DATE:
 CLASSIFICATION: 435
 PRIORITY APPLICATION DATA:
 APPLICATION NUMBER: US 08/043,747
 FILING DATE: 07-APR-1993
 ATTORNEY/AGENT INFORMATION:
 NAME: Oblon, No. 5773243man F.
 REGISTRATION NUMBER: 24,618
 REFERENCE/DOCKET NUMBER: 1126-101-0
 TELECOMMUNICATION INFORMATION:
 TELEPHONE: (703) 413-3000
 TELEFAX: (703) 413-2220
 TELEX: 248855 OPAT UR
 INFORMATION FOR SEQ ID NO: 44:
 SEQUENCE CHARACTERISTICS:
 LENGTH: 5924 base pairs
 TYPE: nucleic acid
 STRANDEDNESS: unknown
 TOPOLOGY: unknown
 MOLECULE TYPE: DNA (genomic)
 FEATURE:
 NAME/KEY: sig_peptide
 LOCATION: 4..69
 FEATURE:
 NAME/KEY: mat_peptide
 LOCATION: 70..4929
 FEATURE:
 NAME/KEY: CDS
 LOCATION: 4..4929
 US-08-447-411-44

Alignment Scores:
 Pred. No.: 1,56e-84 Length: 5924
 Score: 895.00 Matches: 359
 Percent Similarity: 40.84% Conservatives: 296
 Best Local Similarity: 22.38% Mismatches: 673
 Query Match: 12.04% Indels: 276
 DB: 1 Gaps: 56

US-10-020-095-4 (1-1428) x US-08-447-411-44 (1-5924)
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 Db 31 GCTGCTCTATTGATGGTTTCCAGGGTCTTCTCATGGGGCTCTACACCCCTCATACC 90
 QY 33 ProGlyIleArgProGlyGlyAsnValThrIleGlyValGluLeuLeu---GluHis 51
 Db 91 CCTGCTGTTTGGACACACAGACAGACAAATTTTGTGGAGGCCCATGGACACAT 150
 QY 52 CysProSerGlnValThrValLysAla-----GluLeuLeuLysThrAlaSer 67
 Db 151 ACTCCAAAACAGCTTGACATCTTTGTTTCATGATTTTCCAGGAGCAGAGAAACCTTTGTC 210
 QY 68 AsnLeuThrValSerValLeuGluAlaGluGlyValPheGluLysGlySerPheLysThr 87

Db 211 CAAACACAGAGTAGATATGAATCCACAGAGGAGCAATGCTTGTCACT-----CCAACT 261
 QY 88 LeuThrLeuProSerLeuProLeuAsnSerAlaAspGluIleLerGluLeuArgValThr 107
 Db 262 ATAGAGATTCCAGCAAAAGAGTGGAGTCCAGGACATCCAGGCAAAATCAATATGCTGTG 321
 QY 108 GlyArgThrGlnAspGluIleLeuPheSerAsnSerThrArgLeuSerPheGluThrLys 127
 Db 322 CAAGTAACTGCTCCTCAAGTAGATTGGAAGAGGTGTTCTCTTTTCTTACCAGATGAC 381
 QY 128 ArgIleSerValPheIleGlnThrAspLysAlaLeuTyrLysProLysGlnGluValLys 147
 Db 382 -----TTTCGTGTTTATCCAGACAGATAAAGGCATCTATACACAGGGTCTCCAGTACTC 435
 QY 148 PheArgIleValThrLeuPheSerAspPheLysProTyrLysThrSerLeuAsnIleLeu 167
 Db 436 TATCGTGTGTTTCTATGGATCAACACACAGCAAGATGAACAAACTGTGATTGTTGAG 495
 QY 168 IleLysAspProLysSerAsnLeuIleGlnGlnThrLeuSerGlnGlnSerAspLeuGly 187
 Db 496 TTTCACTCCAGAGCAATCTTGTGAGT-----TCTAATTCAGTTGACCTAAAC 546
 QY 188 ValIleSerLysThrPheGlnLeuSerSerHisProIleLeuGlyAspTrpSerIle--- 206
 Db 547 TTTCTTC--TGGCCTTACAAATTTACCAGACCTTGTGAGTTGGGAGCTTGGAGGATTGTG 603
 QY 207 ---GlnValGlnValAsnAspGlnThrTyrTyrGlnSerPheGlnValSerGluTyrVal 225
 Db 604 GCCAAATATGAACATTTCCAGAGAAATATATCTCATATTTTGTATGTCAGAGAAATATGTG 663
 QY 226 LeuProLysPheGluValThrLeuGlnThrPro-----LeuTyrCysSerMetAsn 242
 Db 664 TTGCCAGCTTTGAAGTCCGCTCGCAACCATCAGAGAAGTTTATTATTCATTGACGGCAAT 723
 QY 243 SerLysHisLeuAsnGlyThrIleThrAlaLysTyrThrTyrGlyLysProValLysGly 262
 Db 724 ---GAAATTTCCAGCTGTCTATCACTGCAAGGTACTTGTATGGAGAGAGTGGAAAGT 780
 QY 263 AspValThrLeuThrPheLeuProLeuSerPheTrpGlyLysLysAsnIle----- 280
 Db 781 ---GTGGCCTTTGCTCTTTGGAGTGAAATAGATGATGCTAAAGAGATTTCAGAC 837
 QY 281 -----ThrLysThrPheLysIleAsnGlySerAlaAsnPheSerPheAsnAspGlu 298
 Db 838 TCACCTCAGAGAAATTCGGATTATTGATGGAGATGGGAAAGCACACATAAAAGAGATACA 897
 QY 299 MetLysAsnValMetAspSerSerAsnGlyLeuSerGluTyrLeuAspLeuSerSerPro 318
 Db 898 TTCGTTCTCGATTCCAAATCTCAATGAGCTTTGTTGGGCATCTCTGTATGCACT--- 954
 QY 319 GlyProValGluIleLeuThrValThrGluSerValThrGlyIleSerArgAsnVal 338
 Db 955 -----GTPAACAGTCTATGACAGAAATCAGCAGTATGATGGTAGTCACTGAG 999
 QY 339 SerThrAsnValPhePheLysGlnHisAspTyrIleIleGluPheAspTyrThrThr 358
 Db 1000 CAAAGCGCATTCATATTGTGGCATCTCCCTATCAGATCCACTTCACAAAAACCCCAAA 1059
 QY 359 ValLeuLysProSerLeuAsnPheThrAlaThrValLysValThrArgAlaAspGlyAsn 378
 Db 1060 TATTTCAAGCCAGAGATGCCATATGAATGACGTGATGTATGTACACCCCTGATGGCTCA 1119
 QY 379 GlnLeuThrLeuGluGluArgArgAsnValValIleThrValThrGlnArgAsnTyr 398
 Db 1120 CCAGCT-----GCCCATGTGCGAGTGGTATCATGAGGCGCTTT 1155
 QY 399 ThrGluTyrTrpSerGlySerAsnSerGlyAsnGlnLysMetGluAlaValGlnLysIle 418
 Db 1156 -----CATTCATGGGAACCACTTTGTAGTGATGGGACTGCTGAAGCTC 1197
 QY 419 AsnTyrThrValProGlnSerGlyThrPheLysIleGluPhePheProIleLeuGluAspSer 438
 Db 1198 ATCCTGAACATACCATTTGAATGCTCAA-----AGCCTACCAATCACTGTTAGAAGT 1248

Qy	439	SerGluLeuGlnLeuLysAlaIatyrPheLeuGlySerLysSerSerMetAlaValHisSer	458
Db	1249	AACCATGGAGACCTCCCAAGAGAAGCCAGGCAACAAAGTCCATGACAGCCATAGCCTAC	1308
Qy	459	LeuPheLysSerProSerLysThrTyrlleGlnLeuLysThrArgaspGluAsnIleLys	478
Db	1309	CAAAACCCAGGAGGATCTGAAACTATCTTCATGTAGCCATTATCATCTACAGAGATTAA	1368
Qy	479	ValGlySer-----ProPheGluLeuValValSerGlyAsn-----LysArg	492
Db	1369	CCCGGAGATAACTTACCTGTCAAATTTCAATGTGAAGGCAATGCAATTCACATGAAGCAG	1428
Qy	493	LeuLysGluLeuSerTyrMetValValSerArgGlyGlnLeuValAlaValGlyLys---	511
Db	1429	ATCAAAATATTTCACATACCTCATATTGAATAAAGGGAAGATTTTCAAGGTTCGACGGCAA	1488
Qy	512	-----GlnAsnSerThrMetPheSerLeuThrProGluAsnSerTrpThr	526
Db	1489	CCGAGGAGATGGCGAGATCTGGTGACCATGAATCTGCATATCATCTCCAGATCTCATC	1548
Qy	527	ProLysAlaCysValIleValTyrTyrlleGluaspaspGlyGluIleIleSerAspVal	546
Db	1549	CCCTTCCTCCGGTTTGGGTTACTACTCAAGTGGGAACCAACCAATTTGGCTGATCT	1608
Qy	547	LeuLysIleProValGln-----LeuValPheLys-----AsnLys	558
Db	1609	GTCTGGGTGGATGTGAAGGATACCTGCATGGGAACGTTGGTTGTGAAGAGAGACAATCTA	1668
Qy	559	IleLysLeuTyrTrpSerLysValLysAlaGluProSerGluLysValSerLeuArgIle	578
Db	1669	ATCAAAATG-----CCAGAGCTGCAATGAAATCAAAATG	1704
Qy	579	SerValThrGlnProAspSerIleValGlyIleValAlaValaspLysSerValAsnLeu	598
Db	1705	GAA--GGGGATCCAGGTGCTCGGGTGGTCTGGCTGGCACAAAGCAGATATATGTT	1761
Qy	599	MetAsnAlaSerAsnAspIleThrMetGluAsnValValHisGluLeuGluLeuTyrAsn	618
Db	1762	CTCAATGATAAATATAGATTTAGCAAGTTCAGCAATAGGACACAATAGAAAAAGATGAC	1821
Qy	619	ThrGlyTyrTyrLeuGlyMetPheMetAsnSerPheAlaValPheGlnGluCysGlyLeu	638
Db	1822	TTTGGCTGTACAGCTGGCAGTGGCCAGATAATCTGGGTGTGTTGAAGATGCTGGACTG	1881
Qy	639	TrpValLeuThrAspAlaAsnLeu---ThrLysAsp-----	649
Db	1882	GCCTGTGACACCAAGCAGCTAATCTCAACACCAACACAGAGATCAGCTGCAAAAGTCTCCTCAG	1941
Qy	649	-----	649
Db	1942	CCTGCAATCGGAGGCGTCCAGTCTGTTTTGCTGCTTGACACCAACCAACCAAGCG	2001
Qy	649	-----	649
Db	2002	GCAGATTTTCAGGATCAAGAGACCTGCCTAAATGTGTGAAGATGTATGTCATGATGAGAACCCC	2061
Qy	649	-----	649
Db	2062	ATGGGTACACTTGTGNAAGCGTGCNAANAATACATCCAGGAGGAGATGCTGTAGGCT	2121
Qy	650	-----TyrIleAspGlyValTyrAsp---AsnAlaGluTyrAla	661
Db	2122	GCCTTCCTTGAATGCTGTGCTCATCAAGGGGTCCGAGATGAAACCAACCGGAGAGC	2181
Qy	662	GluArgPheMet-----GluGluAsnGlu---GlyHisIleValAspIleHisAspPhe	678
Db	2182	GAGTTGTTCTGGCAGAGATGATATGAAGATGGTTTCATACAGATAGTATATCATC	2241
Qy	679	SerLeuGlySerSerProHisValArgLysPheProGluThrTrpIleTrpLeu---	697
Db	2242	TCA-----AGGTCGATTTCCCAAGATGGTTGGTGGCTTAA	2280

Qy	698	-----AspThrAsnMetGlyTyArgIleTyrGlnGluPheGluValThr	712
Db	2281	AAGGACTGTGACCGAGGACCTTAAACAGTCACAGGAAATTTCAAGCAAGACAATGTCTTTTAT	2340
Qy	713	ValProAspSerIleThrSerTrpValAlaThrGlyPheValIleSerGluAspLeuGly	732
Db	2341	CTGAGGATTCATCACAACTGGGTGCTGCTGCTGAAGCTTTACACCCCAAGGG	2400
Qy	733	LeuGlyLeuThrThrThrProValGluLeuGlnAlaPheGlnProPhePheIlePheLeu	752
Db	2401	ATC---TGCTGGCTGAACCTTATGAAATAAGAGTCATGAAGACTCTTCTCATGTGACTT	2457
Qy	753	AsnLeuProTyrSerValIleArgGlyGlyGluGluPheAlaLeuGluIleThrIlePheAsn	772
Db	2458	CAAAATGCCATATTCAGTAGTGAAGATGACGACGTGGAGTTCGAGTATCTTCGCAAC	2517
Qy	773	TyrLeuIysAspAlaThrGluValIysValIleIleGluIysSerAspIysPheAspIle	792
Db	2518	TAGTTAACGAGGATTTATGTGCGAGTGAACCTGTATACAAACCAGCGCTTC-----	2571
Qy	793	LeuMetThrSerSerGluIleAsnAlaThrGlyHisGlnGlnThrLeuLeuValProSer	812
Db	2572	-----TGCAGTGTCTCCAAAAAGGACAAAGATACCGACGAGGTTCCCAATTAAGCC	2625
Qy	813	GluAspGlyAlaThrValLeuPheProIleArgProThrHisLeuGly-----GluIle	830
Db	2626	CTGTCTCCAGACGATGACGTTGTGTATAGTCCATTAGACGCAAGGATGCGATGATGT	2685
Qy	831	ProIleThrValThrAlaLeuSerProThrAlaSerAspAlaValThrGlnMetIleLeu	850
Db	2686	GAGATTAAGCAAGTGTCCAGGAAGCGTTGTGTCAGACGGTGTGAGGAAGAACTGAAA	2745
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Db	2746	GTGTACCTGAAGGGTACAGAATCATTTGTGACTATTGTTAACTGGACCCCAAGGCCA	2805
Qy	871	AsnArgLeuGlnSerThr-----LeuIysThrLeuSerPheSerPhe	884
Db	2806	AAAGGAGTTGGTGGAAACACACAGCTAGAAAGTATCAAAAGCCGCAAAATTAGATCACAGATG	2865
Qy	885	ProProAsnThrValThrGlySerGluArgValGlnIleThrAlaIleGlyAspValLeu	904
Db	2866	CCTGCACACAGAAATGAAACCAAGATATATCCAAAGGTGACCCCTGTGGCTCAGATTTAT	2925
Qy	905	GlyProSerIleAsnGly-----LeuAlaSerLeuIleArgMetProTyrGlyCysGly	922
Db	2926	GAATACTCAATTGATGAAGTAAACTCAACCATCTCATATCATCTCTCTGGCTGTGG	2985
Qy	923	GluGlnAsnMetIleAsnPheAlaProAsnIle-----TyrIleLeuAspTyrLeu	939
Db	2986	GAGCAAAATATGATCCGCGATGGCCGACCACTATTATGCCACCTACTCTCTGGACCCACA	3045
Qy	940	ThrIysIysIysGlnLeuThrAspAsnLeuIysGluIysAlaLeuSerPheMetArgGln	959
Db	3046	GACAGTGGAGACTCTCGGCATAAATCCGACGACTGAAGTGTCAATCAGATCGTGACT	3105
Qy	960	GlyTyrGlnArgGluLeuLeuTyrGlnArgGluAspGlySerPheSerAlaPheGlyAsn	979
Db	3106	GGTTATGCCAGCAGATGGTGTCAAGAAGACAGATCATTTCTTATGCGCATTTTCAAAAC	3165
Qy	980	TyrAspProSerGlySerThrTrpLeuSerAlaPheValLeuArgCysPhe---LeuGlu	998
Db	3166	-----CGTGCATCTAGTTCTTGCTTACAGCATATGTCTGTAAGTCTTTGCCATGGCT	3219
Qy	999	AlaAspProTyrIleAspIleAspGlnAsnValLeuHisArgThrTyrThrTrpLeu---	1017
Db	3220	GCCAAATGTTAGCAGCATTAGTTCATGAATCATTTGTGGAGTGTGAGGTGGCTGATT	3279
Qy	1018	LysGlyHisGlnIysSerAsnGlyGluPheThrAspProGlyArgValIleHisSerGlu	1037
Db	3280	CTGACAGGCCAACACACAGATGAGCGGTCAAGAATAATGCCCTGCTACTCTTCGGAACA	3339
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Db 3340 ATGCAGGAGGAAATCAAGGTCTGAGAGAGATATATTAAACAGCTTTCATTCTGGTT 3399
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Db 3400 GCGTTCTTGAATCCAAAACAATCTGCAATGACTATGTCAATAGTCTAGACAGCAGCATC 3459
QY 1069 GlnGluSerIleHisPheLeuGluSerGluPheSerArgGlyIleSerAspAsnTyrThr 1088
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QY 1089 LeuAlaLeuIleThrTyrAlaLeuSerValGlySerProLysAlaLysGluAlaLeu 1108
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Db 3607 -----GAAGAATACATGCTCACACCCACACATTGAAGGCATTCCTATGCC 3654
QY 1149 LeuLeuSerHisPheLeuGlnPheGlnThrSerGluGlyIleProIleMetArgTrpLeu 1168
Db 3655 TTGTTGGCCCTGCTGAAATGAAGAAATTTGATCAAACTGGTCCCATAGTCAGATGGCTG 3714
QY 1169 SerArgGluArgAsnSerLeuGlyGlyPheAlaSerThrGlnAspThrThrValAlaLeu 1188
Db 3715 ACAGATCAGAATTTTATGGGGAACATATGAGCAAAACCCAGCAACATTTATGGCAATTT 3774
QY 1189 LysAlaLeuSerGluPheAlaAlaLeuMetAsnThrGluArg---ThrAsnIleGlnVal 1207
Db 3775 CRAAGCTCTTCTGAATATGAGATTCAGATGCCTTACCCTAAGAGCTTAACCTAGATATT 3834
QY 1208 ThrValThrGlyProSerSerProSerProLeu----- 1218
Db 3835 ACTATTGAATGCCAGATCGAGAAGTACCTATAAGGTACAGAAATTAATTAAGAAATGCT 3894
QY 1219 -----AlaValValGlnPro-----MetAlaValAsnIleSerAlaAsnGly 1232
Db 3895 CTCCTGGCTCGGACGTAGAGACCAACTCAACCAAGACATCACTGTGACAGCATCAGT 3954
QY 1233 PheGlyPheAlaIleCysGlnLeuAsnValValTyrAsnValLysAlaSerGlySerSer 1252
Db 3955 GATGGAAGGCAAAATGATGACATTTTGACATTTCTATAAGCCACAGTTG----- 4002
QY 1253 ArgArgArgSerIleGlnAsnGlnGluAlaPheAspLeuAspValAlaValLysGlu 1272
Db 4003 CAGGAGAGGCAAAATGTTGCAATAAA-----TTTCATCTTAATGTTTCTGTGAA--- 4053
QY 1273 AsnLysAspAspLeuAsnHisValAsp-----LeuAsnValCysThr 1286
Db 4054 ---AACATCCACATTGAATGCAATGGGAGCCAGGAGCCCTCATGCTCAAGATCTGCACA 4110
QY 1287 SerPheSerClyProGlyArgSerGlyMetAlaLeuMetGluValAsnLeuLeuSerGly 1306
Db 4111 AGGTATCTGGGAGAGTTGATTCTACATGACAAATAATTGATATTCTATGCTGATGCTG 4170
QY 1307 PheMetValProSerGluAlaIleSer-----LeuSerGluThrValLys 1321
Db 4171 TTCTCCCTCATGCTGAGACCTTACAGGCTTCTTAAGGATGGACAGATACATCTCC 4230
QY 1322 LysValGluTyrAspHisGlyLysLeuAsn-----LeuTyrLeuAspSer 1336
Db 4231 AGATATGAAAGTTGACAAATAATATGGCTCAGAAAAGTAGCTTTATCATCTTAACATAAG 4290
QY 1337 ValAsnGluThrGln---PheCysValAsnIleProAlaValArgAsnPheLysValSer 1355
Db 4291 GTCTCCACCTCTGAAGATGAATGCCCTTAAAGATTCCTCAAGCATTTTGAAGTTGCG 4350
QY 1356 AsnThrGlnAspAlaSerValSerIleValAspTyrTyrGluProArgGlnAlaVal 1375
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Db 4411 AAGTTTACCATTCCAGATAAAGAACAGGCGCTTCTCAATAAGATATGATTGTTGTAACGTT 4470
QY 1396 CysArgProCysGluAspGlyAlaSerGlySerHisHis----- 1408
Db 4471 TGCCGATCTGCAGGAGAAACCTGTTCTCGTCAACCATCAGGAAAGGATTGATGTTCCA 4530
QY 1409 -----HisSerValIlePheIlePheCysPheLysLeuLeu 1421
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QY 1422 TyrPheMetGlu 1425
Db 4591 CGAATAGAGAA 4602

RESULT 14
US-08-447-411-75
; Sequence 75, Application US/08447411
; Patent No. 5773243
; GENERAL INFORMATION:
; APPLICANT: FRITZINGER, DAVID C.
; APPLICANT: BREDEHORST, REINHARD
; APPLICANT: VOGEL, CARL-WILHELM
; TITLE OF INVENTION: DNA ENCODING COBRA C3, CVF1, AND CVF2
; NUMBER OF SEQUENCES: 81
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: OBLON, SPIVAK, MCCLELLAND, MAIER & NEUSTADT,
; STREET: 1755 S. Jefferson Davis Highway, Suite 400
; CITY: Arlington
; STATE: Virginia
; COUNTRY: U.S.A.
; ZIP: 22202
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/447,411
; FILING DATE:
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/043,747
; FILING DATE: 07-APR-1993
; ATTORNEY/AGENT INFORMATION:
; NAME: Oblon, No. 5773243man F.
; REGISTRATION NUMBER: 24,618
; REFERENCE/DOCKET NUMBER: 1126-101-0
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (703) 413-3000
; TELEFAX: (703) 413-2220
; TELEX: 248855 OPAT UR
; INFORMATION FOR SEQ ID NO: 75:
; SEQUENCE CHARACTERISTICS:
; TYPE: nucleic acid
; STRANDEDNESS: unknown
; TOPOLOGY: unknown
; MOLECULE TYPE: DNA (genomic)
; FEATURE:
; NAME/KEY: CDS
; LOCATION: 3..4001
US-08-447-411-75

Alignment Scores:
Pred. No.: 3,6e-72 Length: 4138
Score: 768.50 Matches: 306
Percent Similarity: 41.88% Conservative: 212
Best Local Similarity: 24.74% Mismatches: 465
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Query Match:	10.46%	Indels:	255	
DB:	1	Gaps:	46	
US-10-020-095-4 (1-1428) x US-08-447-411-75 (1-4138)				
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66	TATCAGATCTACTACAAAACCCCAATAATTTCAAGCCAGGAATGCCATATGAAC	125		
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369	ThrValLysValThrArgAlaAspGlyAsnGlnLeuThrLeuGluGluArgAsnAsn	388		
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126	ACGGTGATGTATCAAAACCTGATGGCTCACAGCTGCC	164		
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389	ValValIleThrValThrArgAsnTyrThrGluTyrTrpSerGlySerAsnSerGly	408		
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165	CATGTGCCAGTGGTATCAGAGGCCATTCATCTGAG	203		
Qy		Db		
409	AsnGlnLysMetGluAlaValGlnLysIleAsnTyrThrValProGlnSerGlyThrPhe	428		
Qy		Db		
204	ACCACTTTGAGTGGAGCTGCTAAGCTCTCTCTGAACACACCAAAATGCTCAA	260		
Qy		Db		
429	LysIleGluPheProIleLeuGluAspSerSerGluLeuGlnLeuLysAlaTyrPheLeu	448		
Qy		Db		
261	-----AGCCTACCGATCTGTAGNACTACATCGGAGACCTCCCAAGAGAACCCAG	314		
Qy		Db		
449	GlySerLysSerMetAlaValHisSerLeuPheLysSerProSerLysThrTyrIle	468		
Qy		Db		
315	GCAATAAAGTCCATGACAGCCACAGCCCTACCAAAACCCAGGAGGATCTGGAAACTATCT	374		
Qy		Db		
469	GlnLeuLysThrArgAspGluAsnIleLysValGlySer	486		
Qy		Db		
375	CATGTACCCATATCATCTACAGAGATTAAACCCGGAGATACTTACCTGTCAATTCAT	434		
Qy		Db		
487	ValSerGlyAsn	502		
Qy		Db		
435	GTGAGGGCAATGCAATTCACCTGAAACAGATCAAAATATTTTCATATCTCATCTGA	494		
Qy		Db		
503	ArgGlyGlnLeuValAlaValGlyLysGlnAsnSer	515		
Qy		Db		
495	AAAGGGAAGATTTCAGGTGTGGCAGCAACACAGGGGAGATGGGAGAAATCTGGTGACC	554		
Qy		Db		
516	Met	534		
Qy		Db		
555	ATGAATCTACATATCATCTCCAGAT	608		
Qy		Db		
535	TyrIleGluAspGlyGluIleIleSerAspValLeuLysIleProValGln	552		
Qy		Db		
609	TACCAAGTGGAAACAATGAATTTGTGGCTGATTCTGTGGGTGGATGTGAAGGATACC	668		
Qy		Db		
553	-----LeuValPheLys	562		
Qy		Db		
669	TGCATGGGAACGTGGTTGTGAAGAGGCGACTTCACAGACAAATCCAAATACAAATG	725		
Qy		Db		
563	TrpSerLysValLysAlaGluProSerGluLysValSerLeuArgIleSerValThrGln	582		
Qy		Db		
726	-----CCAGAGCTGCAATGAAATCAAAATGGAA	761		
Qy		Db		
583	ProAspSerIleValGlyIleAlaValAspLysSerValAsnLeuMetAsnAlaSer	602		
Qy		Db		
762	CCAGGTGCTTGGATGCTGTGGCTGTGGCAGCAAGCAGCAATATGTTCTCAATGATAA	821		
Qy		Db		
603	AsnAspIleThrMetGluAsnValHisGluLeuGluLeuTyrAsnThrGlyTyrTyr	622		
Qy		Db		
822	TATAAGATTAGCAAGCTAAGATATGGGACACATAGAAAAGATGACTTGGCTGTACA	881		
Qy		Db		
623	LeuGlyMetPheMetAsnSerPheAlaValPheGlnGluCysGlyLeuTrpValLeuThr	642		
Qy		Db		
882	CGTGGCAGTGGCAGAAATATCTGGGTGTGTTGAAGATCTCTGGACTGCTCTGCAACC	941		
Qy		Db		
643	AspAlaAsnLeuThr	647		
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942	AGCACTAATCTCAACCAACACAGAGATCAGTGCAGAAAGTGTCTCAGCCTCAAAATCGG	1001		
Qy		Db		

STRANDEDNESS: single
 TOPOLOGY: linear
 MOLECULE TYPE: CDNA
 US-08-662-227-33

Alignment Scores:

Pred. No.: 3,6e-72 Length: 4138
 Score: 768.50 Matches: 306
 Percent Similarity: 41.88% Conservative: 212
 Best Local Similarity: 24.74% Mismatches: 465
 Query Match: 10.46% Indels: 255
 DB: 2 Gaps: 46

US-10-020-095-4 (1-1428) x US-08-662-227-33 (1-4138)

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 DB 66 TATCAGATCTACTTACAAAACCCCAAAATATTTCAGGCAGGAATGCCATATGAAC 125
 QY 369 ThrValLysValThrArgAlaAspGlyAsnGlnLeuThrLeuGluAlaArgAsnAsn 388
 DB 126 ACGGTGATGTTACAAACCTGATGGCTCACCAGCTGCC----- 164
 QY 389 ValValIleThrValThrGlnArgAsnTyrThrGluTyrTrpSerGlySerAsnSergly 408
 DB 165 CATGTCCAGTGTATCAGAGGCCATTCATTCGAG-----GGA 203
 QY 409 AspGlnLysMetGluAlaValGlnLysIleAsnTyrThrValProGlnSerGlyThrPhe 428
 DB 204 ACCACTTTGAGTGGAGCTGCTAAGCTCTCTCTCGAACACACACAAAATGCTCAA--- 260
 QY 429 LysIleGluPheProIleLeuGluAspSerSerGluLeuGlnLeuLysAlaTyrPheLeu 448
 DB 261 -----AGCCTACCGATCACTGTTAGAACTAACCATGGAGACCTCCCAAGAGAACCCAG 314
 QY 449 GlySerLysSerMetAlaValHisSerLeuPheLysSerProSerLysThrTyrIle 468
 DB 315 GCATAAAGTCCATGACAGCCACACGCCCTACCAACCCAGGAGGATCTGGAAACTATCTT 374
 QY 469 GlnLeuLysThrArgAspGluAsnIleLysValGlySer-----ProPheGluLeuVal 486
 DB 375 CATGTACCATTCATCTACAGAGATTAAAGCCGGAGATACTTACTGTCAATTTCAAT 434
 QY 487 ValSerGlyAsn-----LysArgLeuLysGlnLeuSerTyrMetValValSer 502
 DB 435 GTCAGGGGGCAATGCAAAATTCAGTGAACAGACAGATCAATATTTACATACCTCATCTGAAT 494
 QY 503 ArgGlyGlnLeuValAlaValGlyLysGlnAsnSer-----Thr 515
 DB 495 AAAGGGGAAGATTTCAAGTTGGCAGCAACACAGGGGAGATGGGAGAAATCTGGTGACC 554
 QY 516 Met-----PheSerLeuThrProGluAsnSerTrpThrProLysAlaCysValIleValTyr 534
 DB 555 ATGAATCTACATATCACTCCAGAT-----CTCATTCCTCCCTCCGGTTTGGGCTTAC 608
 QY 535 TyrIleGluAspGlyGluIleIleSerAspValLeuLysIleProValGln----- 552
 DB 609 TACCAAGTGGGAACAATGAATATGTGGTGATTCGTCTGGGTGGATGTGAAGGATACC 668
 QY 553 -----LeuValPheLys-----AsnLysIleLysLeuTyr 562
 DB 669 TGCATGGGAACGTTGGTTGGAAAGGAGCGACTTCCAGAGACAAATCGAATACAAATG--- 725
 QY 563 TrpSerLysValLysAlaGluProSerGluLysValSerLeuArgIleSerValThrGln 582
 DB 726 -----CCAGGAGCTGCAATGAAATCAAAATTTGAA---GGGGAT 761
 QY 583 ProAspSerIleValGlyIleValAlaValAspLysSerValAsnLeuMetAsnAlaSer 602
 DB 762 CCAGGTGCTGGATGGTCTGTGGCTGTGGCAAGAGAGAGATATGTTCTCAATGATAA 821
 QY 603 AsnAspIleThrMetGluAsnValValHisGluLeuLeuLysThrGlyTyrTyr 622

DB 822 TATAGATTAGCCAAAGCTAAGATATGGGACACACATAGAAAAGAGTGACTTTGGCTGTACA 881
 QY 623 LeuGlyMetPheMetAsnSerPheAlaValPheGlnGluCysGlyLeuTrpValLeuThr 642
 DB 882 GCTGGCAGTGGCCAGATAAATCTGGGTGTGTTTGAAGATGCTGGACTGGCTCTGCACACC 941
 QY 643 AspAlaAsnLeuThr----- 647
 DB 942 AGCACTAATCTCAACACCAAAACAGAGATCAGTGCAAAAGTGTCTCAGCCTGCAAAATCGG 1001
 QY 647 ----- 647
 DB 1002 AGCGCTCGCAGTTCTGTTTCTGCTTGACAGCAACGCAAGCAAGCGGCACAGTTTCAG 1061
 QY 648 -----LysAspTyrIleAspGlyValTyrAspAsn----- 657
 DB 1062 GATCAAGACCTGCGTAAATGCTGTGAAGATGGCATGATGAAACCCCATGGGCACACT 1121
 QY 658 AlaGluTyrAlaGluArgPheMetGluGluAsnGluGly----- 670
 DB 1122 TGTGAAGCGTGAATAATATCATCCAGAGGGAGATGCTTGTAAAGGTGCTCTCTCGAA 1181
 QY 671 -----HisIleValAspIleHisAsp----- 677
 DB 1182 TGCTGTCTACTATCAAAAGGATCAAGATGACAATAAACGGAGAGCGAGTGTCTTCTG 1241
 QY 678 -----PheSerLeuGlySerSerProHisValArgLys 688
 DB 1242 GCAAGAGTGAATTTGAAGATGATTTATTTGGAGAGGTAAACATCACTCA-----AGGTCT 1298
 QY 689 HisPheProGluThrTrpIleTrpLeu-----AspThr 699
 DB 1299 GATTTTCTGAGAGTGTGTTGCTAATCGAGCAGCTGTCTGAACATCTCTAACAGTAA 1358
 QY 700 AsnMetGlyTyrArgIleTyrGlnGluPheGluValThrValProAspSerIleThrSer 719
 DB 1359 GGGATTTCAAGCAAGATAGTACCTTTTAT-----CTGAGGGATTCATCACAACC 1409
 QY 720 TrpValAlaThrGlyPheValIleSerGluAspLeuGlyLeuGlyLeuThrThr--- 738
 DB 1410 TGG-----GAGTTGCTGGCTGTGGGCTTTTCAACCACCAAA 1445
 QY 739 -----ProValGluLeuGlnAlaPheGlnProPhePheIlePheLeu 752
 DB 1446 GGGATCTGTGGCTGAACCTTATGAAATACAGTCATGAAAGACTTCTTCATTGATCTT 1505
 QY 753 AsnLeuProTyrSerValIleArgGlyGluGluPheAlaLeuGluIleThrIlePheAsn 772
 DB 1506 CAATGCGCTTATTCAGTAGTGAAGATGAGCAGGTGAAATTCGAGCTGTTTGTGTAAC 1565
 QY 773 TyrLeuLysAspAlaThrGluValLysValIleIleGluLysSerAspLysPheAspIle 792
 DB 1566 TACGCTGACAAGGATATTTATGACGATGGAACCTGTTATACAGCCAGCTTCTGCACT 1625
 QY 793 LeuMetThrSerSerGluIleAsnAlaThrGlyHisGlnGlnThrLeuLeuValProSer 812
 DB 1626 GCTTCCACAGAAAGTCAA-----AGATACCGAGAGCAGTGCCTCAATTAAGGCC 1673
 QY 813 GluAspGlyAlaThrValLeuPheProIleArgProThrHisLeuGly-----GluIle 830
 DB 1674 CTGCTCCAGGGCAGTATCGTTTGTATAGTCCCATTAGAGCAAGGATTCGATGATGTT 1733
 QY 831 ProlleThrValThrAlaLeuSerProThrAlaSerAspAlaValThrGlnMetIleLeu 850
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 QY 851 ValLysAlaGluGlyIleGluLysSerTyrSerGlnSerIleLeuLeuAspLeuThrAsp 870
 DB 1794 GTTCTACTGAGGGGAATGGAAGAGTATTGTTACTATTATTGAACTGGAGCCACATACA 1853
 QY 871 AsnArgLeuGlnSerThr-----LeuLysThrLeuSerPheSerPhe 884
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Qy	885	ProProAsnThrValThrGlySerGluA ^g ValGlnIleThrAlaIleGlyAspValLeu	904
Dd	1914	CCTGATACGGAAATAGAACCAAGATTACTATTCAAGGTGATCCTTGGCTCAGACTATT	1973
Qy	905	GlyProSerIleAsnGly-----LeuAlaSerLeuIleArgMetProTyrGlyCysGly	922
Dd	1974	GAAAACTCAATTGATGGAAGTAACAACCATCTCAATTATCACTCCCTTTTGCGCTGGGG	2033
Qy	923	GluGlnAsnMetIleAsnPhe---AlaProAsnIle-----TyrIleLeuAspTyrLeu	939
Dd	2034	GAGCAAAAATATGATCCGCATGACTCGCACCATGTTATGCCACTTACTTCCTGGACACCACA	2093
Qy	940	ThrLysIleLysGlnLeuThrAspAsnLeuLysGluLysAlaLeuSerPheMetArgGln	959
Dd	2094	CAGCAGTGGGAGACTCTCGGCATAAATCGCAGGACTGAAGCTGTCAATCAGATCATGACT	2153
Qy	960	GlyTyrGlnArgGluLeuLeuTyrGlnA ^g GluAspGlySerPheSerAlaIlePheGlyAsn	979
Dd	2154	GGTTATGCCAGCAGTTGGTGTACAGAAGAACGACACCATTCCTCATCAGCATTTTACAAC	2213
Qy	980	TyrAspProSerGlySerThrTrpLeuSerAlaPheValIleUArgCysPhe---LeuGlu	998
Dd	2214	-----AGTGCATCTAGTTCTTGGCTTAACGACATATGTTGTAAAAATCTTTGCCCTGGCT	2267
Qy	999	AlaAspProTyrIleAspIleAspGlnAsnValLeuHisHsiargThrTyrThrTrpLeu---	1017
Dd	2268	GCCAAAATTGTAAAGACATTAACCATGAATCGTTTGTGAGGTATGAGGTGGCTGATT	2327
Qy	1018	LysGlyHisGlnLysSerAsnGlyGluPheTrpAspProGlyArgValIleHisSerGlu	1037
Dd	2328	CTGAACAGGCAACGACAGATGGAGTGTTCAGAGAAAACGCCCTGTACTTTTTTGGAAACA	2387
Qy	1038	LeuGlnGlyGlyAsnLysSerProVal-----ThrLeuThrAlaTyrIleValThr	1054
Dd	2388	ATGCAGGAGGCATTCGAGTGTGAACACGAGGATCTTTACAGCTTTTCATTCGGTT	2447
Qy	1055	SerLeuLeuGlyTyrArzGlyTyserGlnProAsnIleAspValGlnGlusertIleHisPhe	1074
Dd	2448	CGGTTGTGAATCCAGATCAATC-----TGCAATGCATATATCAATATT	2492
Qy	1075	LeuGluSerGluPheSerArzGly-----IleSer	1084
Dd	2493	CTGACAGCAGCATCAGTAAGGCCACAGATATTATTACTCAAAGTAGTAGAAACTGCACA	2552
Qy	1085	AspAsnTyrThrLeuAlaLeuIleThrTyrAlaLeuSerSerValGlySerProLysAla	1104
Dd	2553	AGGCCTTACACTACAGCCCTCACAGCCTATGCTTTTGGCT-----GCT	2594
Qy	1105	LysGluAlaLeuAsn-Met-----LeuthrTrpArgAlaGluGlnGluGlyMetG1	1122
Dd	2595	GCAGAACGACTCAATATGATGACGGGTACTCATGCGACGCATCAACAGGAAGGA-----	2646
Qy	1122	nPheTrpValSerSerGluSerLysLeuSerAspSerTrpGlnProArgSerLeuAspI1	1142
Dd	2647	-----ATCGTTGGGAGAACCTAACGCCACACCCATAAC-AT	2683
Qy	1142	eGluValAlaalaTyrAlaLeuLeuSerHisPheLeuGlnPheGlnThrSerGluGlyI1	1162
Dd	2684	TGAAGGCATTCCTATGCTTTGTTGGCCCTGCTCAAAATGAAGAAATTTGTTGAGGCCGG	2743
Qy	1162	eProIleMetArgTrpIleuSerArzGlnArzAsnSerLeuGlyGlyPheAlaserThrG1	1182
Dd	2744	TCCTGTAGTCCAATGGCTGTATGATCAGCAATATTATTGGGGGAACATATGGACAAACCCA	2803
Qy	1182	nAspThrThrValAlaLeuLysAlaLeuSerGluPheAlaAlaLeuMetAsnThrGluAr	1202
Dd	2804	AGCAACAGTTATGATGTTTCAAGCTCTTGCTGATATATCAGATTTCAGATGCCATCCATAA	2863
Qy	1202	g----ThrAsnIleGlnValThrValThrGlyProSerSerProSerPro-----	1217
Dd	2864	GGACTTAACTTAGATATATTAATTGAACTGCCAGATCGGAAGTACTCTTAAGGTACAG	2923

Qy	1218	-----LeulalavalValGlnProMetAlaValAsn-----	1222
Db	2924	AATTAATTGAAATGCTCTCTCTGCTCAGACAGTAGAGACCAAACTCAGGAGACTT	2983
Qy	1228	-----IleSerAlaAsnGlyPheGlyPheAlaIleCysGlnLeuAsnValValTyrAsnVa	1246
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Qy	1246	llysAlaSerGlySerSerArgArgArgSerIleGlnAsnGlnGluAlaPheAspLe	1266
Db	3044	ACAAATG-----AGGAGAGATGCAAAATGTTGCCAACAAA-----TTCCATCT	3085
Qy	1266	uAspValAlaVal-----LysGluAsnLysAspAspLeuAsnHi	1279
Db	3086	TGATGTTTCTGTTCAAACACGCTCCAGTTTGAATTTAAAGAGGCAAGGAGGCCAAGGGAGC	3145
Qy	1279	sValAspLeuAsnValCysThrSerPheSerGlyProGlyArgSerGlyMetAlaLeuMe	1299
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Qy	1299	tGluValAsnLeuSerGlyPheMetValProSerGluAlaIleSer---LeuSerGl	1318
Db	3206	TGATGTTTCTATGCTGACTGTTTGTTCCTGATATGAAAGACCTTACGAGGCTTCTAA	3265
Qy	1318	uThrValLysLys-----ValGluTyrAspHis-----GlyLy	1329
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Db	3326	TGTTATCATTTACTATGACAAAGGCTCCCACTCTGAAGATGAAATGCTGCACCTTAAAGT	3385
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Db	3386	TCTCAAGCATTTTGAAGTTGGCTTCATTCAGCCAGGATCAGTCAAGGTGTACAGCTACTA	3445
Qy	1368	rGluProArgGlnAlaValArgSerTyrAsnSerGluValLysLeuSerSerCysAs	1388
Db	3446	CAATCTAGATGAAAATGTACCAAGATCTACCATCCAGATGAACCAACAGGCTTCTCAA	3505
Qy	1388	pLeuCysSerAspValGlnGlyCysArgProCysGluAspGlyAlaSer	1404
Db	3506	TAAGATATGCTGTGGTACGTTTCCGATGTGCAAGAAACCTGTGTTCC	3554

Search completed: August 18, 2004, 05:37:38
Job time : 718 secs

GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: August 10, 2004, 19:31:34 ; Search time 57 Seconds
(without alignments)
7858.583 Million cell updates/sec

Title: US-10-020-095-4
Perfect score: 7348
Sequence: 1 MQGPPLTAHLLCVCTAAL.....HSSVIFCFKLLYFMELWL 1428

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 1291235 seqs, 313682936 residues

Total number of hits satisfying chosen parameters: 1291235

Minimum DB seq length: 0
Maximum DB seq length: 2000000000
Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : Published Applications AA.*

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- 18: /cgn2_6/ptodata/2/pubpaa/US60_PUBCOMB.pep.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match %	Length	DB ID	Description
1	3360	45.7	665	15	US-10-108-260A-3396
2	2962.5	40.3	596	12	US-10-112-944-404
3	1854.5	25.2	1508	15	US-10-369-493-5314
4	1850	25.2	1519	15	US-10-369-493-5313
5	1628.5	22.2	336	15	US-10-264-237-2445
6	1592	21.7	352	12	US-10-276-774-1951
7	1542.5	21.0	1799	15	US-10-085-198-30
8	1539.5	21.0	1885	15	US-10-085-198-28
9	1529.5	20.8	1927	15	US-10-085-198-26
10	1491	20.3	1476	12	US-09-972-211-69
11	1491	20.3	1476	12	US-10-096-625-69
12	1441	19.6	1474	12	US-09-972-211-65
13	1441	19.6	1474	12	US-10-096-625-65
14	1441	19.6	1474	12	US-10-608-397-15
15	1441	19.6	1474	13	US-10-052-817-2

16	1441	19.6	1474	14	US-10-292-081A-15	Sequence 15, Appl
17	1440	19.6	1474	9	US-09-873-403-5	Sequence 5, Appl
18	1440	19.6	1474	12	US-09-972-211-66	Sequence 66, Appl
19	1440	19.6	1474	12	US-10-170-385-405	Sequence 405, App
20	1440	19.6	1474	12	US-10-096-625-66	Sequence 66, Appl
21	1440	19.6	1474	12	US-10-608-397-10	Sequence 10, Appl
22	1440	19.6	1474	12	US-10-608-397-12	Sequence 12, Appl
23	1440	19.6	1474	12	US-10-608-397-13	Sequence 13, Appl
24	1440	19.6	1474	12	US-09-750-972-5	Sequence 5, Appl
25	1440	19.6	1474	14	US-10-292-081A-10	Sequence 10, Appl
26	1440	19.6	1474	14	US-10-292-081A-12	Sequence 12, Appl
27	1440	19.6	1474	14	US-10-292-081A-13	Sequence 13, Appl
28	1440	19.6	1474	15	US-10-331-496A-38	Sequence 38, Appl
29	1437.5	19.6	1508	10	US-09-756-247-4	Sequence 4, Appl
30	1436	19.5	1458	12	US-10-096-625-200	Sequence 200, App
31	1433	19.5	1450	10	US-09-756-247-23	Sequence 23, Appl
32	1433	19.5	1491	10	US-09-756-247-25	Sequence 25, Appl
33	1428	19.4	1500	12	US-10-608-397-9	Sequence 9, Appl
34	1428	19.4	1500	14	US-10-292-081A-9	Sequence 9, Appl
35	1421.5	19.3	1492	11	US-09-981-151A-10	Sequence 10, Appl
36	1421.5	19.3	1492	12	US-09-972-211-2	Sequence 2, Appl
37	1421.5	19.3	1492	12	US-10-096-625-2	Sequence 2, Appl
38	1419	19.3	1451	10	US-09-756-247-24	Sequence 24, Appl
39	1417.5	19.3	1450	12	US-10-037-417-113	Sequence 113, App
40	1413.5	19.2	1450	12	US-09-972-211-67	Sequence 67, Appl
41	1413.5	19.2	1450	12	US-10-096-625-67	Sequence 67, Appl
42	1412.5	19.2	1472	12	US-09-972-211-68	Sequence 68, Appl
43	1412.5	19.2	1472	12	US-10-096-625-68	Sequence 68, Appl
44	1406.5	19.1	1476	12	US-10-037-417-114	Sequence 114, App
45	1395	19.0	1473	12	US-10-037-417-112	Sequence 112, App

ALIGNMENTS

RESULT 1
US-10-108-260A-3396
; Sequence 3396, Application US/10108260A
; Publication No. US20040005560A1
; GENERAL INFORMATION:
; APPLICANT: HELIX RESEARCH INSTITUTE
; TITLE OF INVENTION: No. US20040005560A1e1 full length cDNA
; FILE REFERENCE: HL-A0106
; CURRENT APPLICATION NUMBER: US/10/108,260A
; CURRENT FILING DATE: 2002-03-27
; NUMBER OF SEQ ID NOS: 5458
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 3396
; LENGTH: 665
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-108-260A-3396

Query Match 45.7%; Score 3360; DB 15; Length 665;
Best Local Similarity 100.0%; Pred. No. 2.4e-267;
Matches 657; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy	1	MQGPPLTAHLLCVCTAALAVAPGPRFLVTAPGIIIRPGNVITGVLELHCPQSVTVKA	60
Db	1	MQGPPLTAHLLCVCTAALAVAPGPRFLVTAPGIIIRPGNVITGVLELHCPQSVTVKA	60
Qy	61	ELLKTASNLTVSVLEAEGVFEKSGFKTLTLPSLNLSADEIYELRVGTGRTODELIFNST	120
Db	61	ELLKTASNLTVSVLEAEGVFEKSGFKTLTLPSLNLSADEIYELRVGTGRTODELIFNST	120
Qy	121	RLSFETKRISVFIQTDKALYKPKQEVKFRIVTLFSDFKPYKTSNLILKDPKSNLIQOWL	180
Db	121	RLSFETKRISVFIQTDKALYKPKQEVKFRIVTLFSDFKPYKTSNLILKDPKSNLIQOWL	180
Qy	181	SCQSDLGWISKTFOLSHPIIGDWSIQVNDQIYQSFQVSEYLPKFEVTLQTPLYCS	240
Db	181	SCQSDLGWISKTFOLSHPIIGDWSIQVNDQIYQSFQVSEYLPKFEVTLQTPLYCS	240

Qy	241	MNSKHLNGHITAKYTYGKPVKGDVTLTFLPLSPFWGKKKNIKTFKINGSANFSFNDEEMK	300
Db	241	MNSKHLNGTITAKYTYGKPVKGDVTLTFLPLSPFWGKKKNIKTFKINGSANFSFNDEEMK	300
Qy	301	NWMDSSNGLSEYLDLSSPGPEIILTTVTESVTGISRNVSTNVFPKQHDYIIIEFPDYTTVL	360
Db	301	NWMDSSNGLSEYLDLSSPGPEIILTTVTESVTGISRNVSTNVFPKQHDYIIIEFPDYTTVL	360
Qy	361	KPSLFTATVKVTRADGNQLTLERRNNVITVTQRNYTEYWSGNSGNORMEAVQKINY	420
Db	361	KPSLFTATVKVTRADGNQLTLERRNNVITVTQRNYTEYWSGNSGNORMEAVQKINY	420
Qy	421	TVPSQSTFKIEPPILEDSEIQLKAYFLGSKSSMAVHSLFKSPSKTYIQLKTRDENIKVG	480
Db	421	TVPSQSTFKIEPPILEDSEIQLKAYFLGSKSSMAVHSLFKSPSKTYIQLKTRDENIKVG	480
Qy	481	SPEFLVWSGNKRLKELSYMWVSRGOLVAVGKONSTMFSLTPENSWTPKACVIVYIEDDG	540
Db	481	SPEFLVWSGNKRLKELSYMWVSRGOLVAVGKONSTMFSLTPENSWTPKACVIVYIEDDG	540
Qy	541	EIISDVLKIPVQLVFNKIKILYWSKVKAEPSEKVSRLRISVTQPDLSIVGIIVAVDKSVNLXN	600
Db	541	EIISDVLKIPVQLVFNKIKILYWSKVKAEPSEKVSRLRISVTQPDLSIVGIIVAVDKSVNLXN	600
Qy	601	ASNDITMENVWELELYNTGYLGNFMNSPAVFOCGGLWLTDLANTLKDYIDGVND	657
Db	601	ASNDITMENVWELELYNTGYLGNFMNSPAVFOCGGLWLTDLANTLKDYIDGVND	657
RESULT 2			
US-10-112-944-404			
; Sequence 404, Application US/10112944			
; Publication No. US20040048249A1			
; GENERAL INFORMATION:			
; APPLICANT: Tang, Y. Tom			
; APPLICANT: Yang, Yonghong			
; APPLICANT: Wang, Gezhi			
; APPLICANT: Zhang, Jie			
; APPLICANT: Ren, Feiyang			
; APPLICANT: Xue, Aidong J.			
; APPLICANT: Wang, Jian-Rui			
; APPLICANT: Wehrman, Tom			
; APPLICANT: Ghosh, Malabika			
; APPLICANT: Wang, Dunrui			
; APPLICANT: Zhao, Qing Ai.			
; APPLICANT: Wang, Zhiwei			
; TITLE OF INVENTION: No. US20040048249A1el Nucleic Acids and			
; TITLE OF INVENTION: Secreted Polypeptides			

```

RESULT 3
US-10-369-493-5314
; Sequence 5314, Application US/10369493
; Publication No. US2003023675A1
; GENERAL INFORMATION:
; APPLICANT: Cao, Yongwei
; APPLICANT: Hinkle, Gregory J.
; APPLICANT: Slater, Steven C.
; APPLICANT: Goldman, Barry S.
; APPLICANT: Chen, Xianfeng
; TITLE OF INVENTION: EXPRESSION OF MICROBIAL PROTEINS IN PLANTS FOR PRODUCTION OF
; TITLE OF INVENTION: PLANTS WITH IMPROVED PROPERTIES
; FILE REFERENCE: 38-10(52052)B
; CURRENT APPLICATION NUMBER: US/10/369,493
; CURRENT FILING DATE: 2003-02-28
; PRIOR APPLICATION NUMBER: US 60/360,039
; PRIOR FILING DATE: 2002-02-21
; NUMBER OF SEQ ID NOS: 47374
; SEQ ID NO 5314
; LENGTH: 1508
; TYPE: PRT
; ORGANISM: Caenorhabditis elegans

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US-10-276-774-1951
; Sequence 1951, Application US/10276774
; Publication No. US20040053245A1
; GENERAL INFORMATION:
; APPLICANT: Hyseq, Inc.
; TITLE OF INVENTION: Tang, Y, Tom et al
; FILE REFERENCE: 21272-030
; CURRENT APPLICATION NUMBER: US/10/276,774
; PRIOR FILING DATE: 2002-11-18
; PRIOR APPLICATION NUMBER: 09/560,875
; PRIOR FILING DATE: 2000-04-27
; PRIOR APPLICATION NUMBER: 09/496,914
; PRIOR FILING DATE: 2000-02-03
; NUMBER OF SEQ ID NOS: 2700
; SOFTWARE: Custom
; SEQ ID NO 1951
; LENGTH: 352
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-276-774-1951

Query Match          21.7%; Score 1592; DB 12; Length 352;
Best Local Similarity 92.2%; Pred. No. 4.2e-12;
Matches 319; Conservative 6; Mismatches 3; Indels 18; Gaps 2;

QY 1067 DVESIHFLSEFSRSGISDNVTYLIATIIYALSSVGSPrAKAALNMLTWRAQEGGMQFVWS 1126
DB 2 EVESIHFLSEFSRSGISDNVTYLIATIIYALSSVGSPrAKAALNMLTWRAQEGGMQFVWS 61

QY 1127 SESKLSDSWQPSRLDIEVAAYALLSHFLQFTSEGIPIMRWLGRQNSLGGFASTQDTTV 1186
DB 62 SESKLSDSWQPSRLDIEVAAYALLSHFLQFTSEGIPIMRWLGRQNSLGGFASTQDTTV 121

QY 1187 ALKALSEFAALMTERNIQVTWTPGSPSPSL-----AVQPM-----AVNI 1228
DB 122 ALKALSEFAALMTERNIQVTWTPGSPSPVKFLIDTHNRLLILQTAEADGTANGSVSI 181

QY 1229 SANGFGFAICQLNVVYNVVKASGSSRRRSRISQNEAFDLVAVKENKDDLNVLDINVCTSF 1288
DB 182 SANGFGFAICQLNVVYNVVKASGSSRRRSRISQNEAFDLVAVKENKDDLNVLDINVCTSF 241

QY 1289 SGFGRSGMALMEVNLISGFVWPSEAISLSTVTKVVDHGKMLNYLDSVNETQFCVNIPA 1348
DB 242 SGFGRSGMALMEVNLISGFVWPSEAISLSTVTKVVDHGKMLNYLDSVNETQFCVNIPA 301

QY 1349 VRNFKVSNTODASVIVDYVEPRQAVRSYNSEVKLSSCDLCSDVQ 1394
DB 302 VRNFKVSNTODASVIVDYVEPRQAVRSYNSEVKLSSCDLCSDVQ 347

RESULT 7
US-10-085-198-30
; Sequence 30, Application US/10085198
; Publication No. US20040009907A1
; GENERAL INFORMATION:
; APPLICANT: Alsebrook et al.
; TITLE OF INVENTION: Proteins and Nucleic Acids Encoding Same
; FILE REFERENCE: 21402-279
; CURRENT APPLICATION NUMBER: US/10/085,198
; CURRENT FILING DATE: 2002-02-25
; PRIOR APPLICATION NUMBER: 60/271,646
; PRIOR FILING DATE: 2001-02-26
; PRIOR APPLICATION NUMBER: 60/276,401
; PRIOR FILING DATE: 2001-03-16
; PRIOR APPLICATION NUMBER: 60/311,981
; PRIOR FILING DATE: 2001-08-13
; PRIOR APPLICATION NUMBER: 60/312,858
; PRIOR FILING DATE: 2001-08-16
; PRIOR APPLICATION NUMBER: 60/271,840
; PRIOR FILING DATE: 2001-02-27
; PRIOR APPLICATION NUMBER: 60/277,324
; PRIOR FILING DATE: 2001-03-20

```


382 QI-----KAEITPKDNIYTSVVSGRLVGFREISIPTSAOHVWLETK 424
445 AYFGSK-----SSMAVHSLFKSPSKTYIOLKTRDENIKYGVSPFELVSGNKLK-E 495
425 VMALNGKPVGAQVLPVSLSLGSWY-SPSQCYLOQLPPSHPLQVGEAYFSVKSTCPNFT 483
496 LSYMVVSRGOLVAVGKO-----N 513
484 LYTEVARGNIVLSGQQAHTTQORSKRAAPALEKPIRLTHLSETPPPAPEADVCVT 543
514 STMFSLTPENSWTPKACVIYVYIEDGEEIISDLVKIPVQLVFNKIKLYWSKVYKAPSEK 573
544 SLHLAVTP--SMVPLGSLLVYVRENGEGVADSLQPAVETFFENQSVTVYSANETQGEV 601
574 VSLRISVQPDSDISGIVAVDKSVNLMNASNDITWENVVHELELYNTG-----620
602 VDLRIRAAAR-GSCVCVAAVDKSVYLRSGFRLTPAQVQLEDDYVSDSFGVSRDGPFW 660
621 -----YYLGMFNMSFAVFOECGLWLTD--ANLTKDYIDGVYDVAEYAE 663
661 WAGITAOQRRSSVFPFPWGITKDSGFAFTETGLVWMTDRVSLNHRQDGLY--TDEAVP 718
664 FMENEGHIVDIHDFSLGSPH-----VRKHPPETWIMLDTNMGVRIYQ-EFEVTPD 715
719 AFQPHGSLV-----AVAPSRHPPTREKRTTFPPTWIMHCLNISDPGEGTSLVKVPD 773
716 SITSWATGFIWISDLGLTTPVELQAFQPFIFLNLPSYVIRGEERALEITINYLK 775
774 SITSWGEAVALTSQGLGI-APSLKTKFPFVDFMLPALLIRGEQVPIKPSVYNYMG 832
776 DATEV--KVIEKSKDFDILMTSEINATCH-----QOTLLVPSBDGATVLPPIRPTH 827
833 TCAEVYMKLSVPKGIQF-----VGHGPKRHVTWKMCVAPGEAPFIWVLVSFSDL 881
828 GEIPITVIALS-----PTASDVTOMLYKAEIGKESYSQ 862
882 GLNNITAKALAYGNTCCRDGRSKKPEENHADRPIGVHDVRRSVMVVEAGVPRAYTY 941
863 SIL-----LDLT-----DNRL-----873
942 SAFFCPSERVHISTPNKYEFYQVRLPLRFDVAVRAHNDARVALSSGPDAGMIEIV 1001
874 -----OSTLKLTSF-----882
1002 LGGHQNTSRWISTSKGEPVASAHTAKILSDWBERTFWISWRGLLIQVGHGPPSPNESVI 1061
883 -----SPPNTVTSERVQIT 898
1062 VANTLPPPEVQIGTSGWNGEFAIRWKMEVDESYSSEAFVLGVPHGAIPGSEBRTAS 1121
899 AIGDVLGPIINGLASLIRMPYCGEQNMINFAPNIYILDYLTKKQLTDLNKEKALSFVR 958
1122 IIGDVMGPTLNLNLRLPFGCGEQNMIFAPNVFLVKYLOKTQOLSPEVERETTDYLV 1181
959 QGYORELLYCREDSFSAFNGYDPSGTSWLSAFVLCFLFEADPYIIDQVNLHRTTWLX 1018
1182 QGYORQTYRKQDGSYAFGERDASGSMMLTAVLKSFAQARSFIFVDPRELAASKSMTI 1241
1019 GHQKNGEFDGPRGVHSHLQGNKSPVLTAYIVTSL--GYRKYQPNIDVOESIHPLF 1076
1242 QQQAQDGSFLAVGRVNLKDIQGGIHGIVPLTAYVVVALLETGTASEEERGSTDKASHFLE 1301
1077 SEFSRGISDNYTALITYALSVSGSPAKALNMLTWRAEQEGMGQFVSSSEKSLDSQW 1136
1302 SAAPLAW-DPYSICALTYALTLLRSAPAEALRSLAIRMDGVTH-----SLNSWD 1355
1137 PR-----SLDIEVAVALLSHFLQFOTSEGIPIRMLWLSGRNSLGGPAS 1180
1356 VDKGTFLSFSDRSVQSUSVSEVENTAYALLTYLLGDVAALPVVKNLSCQORNALGGFS 1415
1181 TQDTVALKALSFAAL-----MNTERTNIQVTVTG--PSPFS 1216
1416 TQDTCVALQALAEVAILSVAGGINLATVSLASTNLDYCEPTELHRTNQKVLQAAPISLPT 1475

QY 1217 PLAVVQPMVAVNISANGFGAICQLNVVNVX---ASGSSRRRRSTONOE-----1262
Db 1476 GLFV-----SAKGDGCLMQIDVTYVNDPDPVAKPAFQLLIVSLQBPEAQGRPPMPAS 1527
QY 1263 -----AFDLDDVAVKENKIDLNHVDLNVCTSPSGRSGMALVEVNLISGFMVPS 1311
Db 1528 AAEGRGDWPPADDDDDPAADQHHQYK--VMLEVCRTWLHAGSSNMAVLEVLPSGFRADI 1586
QY 1312 EALSSET-----VKKVEYDHGKINLYLDSV-NETQFCVNI PAVRNFKVSNTOASVS 1363
Db 1587 E--SLEQLLLDKHMKRYEVAGRRVLFYFDBIPSRCLTCVFRALRECVVGRTSALPVS 1644
QY 1364 IVDYVEPRQAVRSVNSEV-----KLSSCDLCSQVQ-----GCRCEGASGSHHS 1410
Db 1645 VDYVEPAFEATRFYVNSTHSPFLABELCAGFACNEVERAPARGPWFPGESGPAVABEG 1704
QY 1411 SVI 1413
Db 1705 AA 1707

RESULT 9
US-10-085-198-26
; Sequence 26, Application US/10085198
; Publication No. US20040009907A1
; GENERAL INFORMATION:
; APPLICANT: Alsobrook et al.
; TITLE OF INVENTION: Proteins and Nucleic Acids Encoding Same
; FILE REFERENCE: 21402-279
; CURRENT APPLICATION NUMBER: US/10/085,198
; CURRENT FILING DATE: 2002-02-25
; PRIOR APPLICATION NUMBER: 60/271,646
; PRIOR FILING DATE: 2001-02-26
; PRIOR APPLICATION NUMBER: 60/276,401
; PRIOR FILING DATE: 2001-03-16
; PRIOR APPLICATION NUMBER: 60/311,981
; PRIOR FILING DATE: 2001-08-13
; PRIOR APPLICATION NUMBER: 60/312,858
; PRIOR FILING DATE: 2001-08-16
; PRIOR APPLICATION NUMBER: 60/271,840
; PRIOR FILING DATE: 2001-02-27
; PRIOR APPLICATION NUMBER: 60/277,324
; PRIOR FILING DATE: 2001-03-20
; PRIOR APPLICATION NUMBER: 60/286,096
; PRIOR FILING DATE: 2001-04-21
; PRIOR APPLICATION NUMBER: 60/299,695
; PRIOR FILING DATE: 2001-06-20
; PRIOR APPLICATION NUMBER: 60/315,614
; PRIOR FILING DATE: 2001-08-29
; PRIOR APPLICATION NUMBER: 60/272,405
; PRIOR FILING DATE: 2001-02-28
; Remaining Prior Application data removed - See File Wrapper or PALM.
; NUMBER OF SEQ ID NOS: 653
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 26
; LENGTH: 1927
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-085-198-26

Query Match 20.8%; Score 1529.5; DB 15; Length 1927;
Best Local Similarity 26.8%; Pred. No. 1.2e-115;
Matches 494; Conservative 258; Mismatches 559; Indels 529; Gaps 57;

QY 5 PLLTAHLLVCV---TAALAVAPGPRFLVTPAGTIIRPGNVNIGVLELHCPQSVTVKA 60
Db 8 PLLPLLLLLSARDGVRAAQPAQ--YLIAAPSVFRAGVEEIVSVTIF-NSPREVTVQA 64
QY 61 ELLKTASNLTVSLEAEG-VFEKGSFK-----TLTLPSPILNSADEIY 102
Db 65 QLVAGQE----PVQSQAILDKGTIKLHTVLTSTGSLPILALLIGGDLSSLSFLW 120

103 E-----LRVTR-----TODEILFSNSTRLSFETKISVFIQTDKAL 139
121 PVLRYFQKQGVPTGLRGOALLKVGSGWQAEGBPLFHNQTSVTVDRGASVFIQTDKPV 180
140 YKPKQEVKFRIVLTFSPDKPKYSNLNLIKDPKSNLIQWLS--QQSDGLGVISKTFLSSH 198
181 YRPOHRLI1SIFVSPNLRVNEKLEAYILDPGRSMIEWHLKPFCCGTTNMFPLSDQ 240
199 PILGDSIQOVNDQTYQGFQVSEYVLPKFEVTLQTPLYCSMNSXHLNITIAKTYGK 358
241 PVLGEWIFVEMQCHANKSEVQKYLPAFELLIDPPRYIQDLDACETGVREARYFGK 300
259 PVKGD--VTLTFLPLSPWKK--KNITKTPKINGSANFSEDEMNKNDSSNGLSEYLD 314
301 PVAGALMINVTNGVGYSHVEGRVPLRTTKILGSRDFDICVRDM-----IP 347
315 LSSP-----GPVEILLTVTESVTGFSRNVSTNVFKQHDYIIEFDDVTV----- 359
348 ADVEHFRGRVS IAWMT--SVDSGQ-----VAFDDSTPVQRQLVDIYYSK 392
360 -----LRPSLNFTATVKVTRADGNQLTLEBRNNVITVTORNYTEYWSGNSGNQKMEA 414
393 DTRKQKFGLAYVGVKVELSPDGS-----AEGVTVOI-----KAEL 429
415 VOKIN-VT---VPSGTFKIEFPLEDSB---LQKAYELGSK-----SSMAVHSL 459
430 TPKDNITVSEVVSORGVLGVEIPIPTSAOHVLETKVMALNGKPVGAQVLPYLSLGSW 489
460 FKPSKTYIOLKTRDENIKGSPPELVVSGNKRILK-ELSTMVYSRGOLVAVGRQ----- 512
490 Y-SFSQCYLQPPSHPLQGEAYEYVSKTGPCNFTLYEVAAGNIVLSGQPAHTTQ 548
513 -----NSTMFSITPNSWTPKACVIVYI 536
549 QRSKRAAPALEKPIRLTHLSETEPPPAEABVDVCTSLHLAVTP--SMVPLGRLLVFFV 606
537 EDGEITSDVLKI PVQLVFNKIKLYSKVKAEPSEKVSIRISVTPDSITGVIVAVDKSV 596
607 RENEGVADSLQFAVEFFENQVSVTSANETQGEVVDLIRAAAR--GSCVCVAAVADKSV 665
597 NLNANSDITMENVHELELYNTG-----YVLGMFM 627
666 YLLRSGLFPLPAQVFBQLELYDVSDFGVSREDGFFWAGLTAQRRRRSVFFPWPWGITX 725
628 NSFAVFOEGLVWLTD-ANLTKVDYDGVNDAEVAERFMEENEGHIVDIDHDFSLGSSPH- 685
726 DSGFAFTETGLVMDRVSLNHRQDGLY--TDEAVPAFQHTGSLV-----AVAFSRHP 778
686 -----VRKHPPETWILDTNMGRIYQ-BFEVTVPSDITSWVATGFEVISEDIGLGLTTT 738
779 PRTEKRKXTEFPETWIWHLNIDSPSGEGLTSVKVPDSITSWVGEAVALSTSQGLGI-AE 837
739 PVELQAOQPPFIPLNLPYSVIRGEPALEITIFNLYKDATEV--KVIEKSKDFDILMWS 796
838 PSLKTKFPFVDFMPLPALIRGEQVKIPUSVYNYMTCAEVYMKLSVPRKGIQF----- 891
797 SEINATGH-----QOTLLVPSEDCATVLPPIRTHLGEIPITVTLAS----- 838
892 -----VGHPGKHVTKKVCNAPGAEPIMVWVLSFSLGLNITAKALAYGDTNCCRDGRS 946
839 -----PTASDAVTOMLLVKAEGIEKYSOSIL----- 865
947 SKHPEENHADRVPVIGVDHVRSSVWVWAEVGPRAITYTSAPFCPSERVHISTPNKPYFYV 1006
866 ---LDLT-----DNRL-----Q 874
1007 QRPRLTRFDVAVRAHNDARVALSSGQCDTAGMIEIVLGGHONTRSWISTSKYGEPVASA 1066
875 STLKTLPS----- 882
1067 HTAKILSDEPRTFWISWRGGGLIQVGHGPEPSNESIVAWTLFRPPEVQFIFSTGWGSM 1126
883 -----SFPNTVTGSEVRQIITAIGDVLGPSINGLASLIRMPYGC 921

1127 GEFRWRKMEVDESYSEAFITLVGPHGAIPGSEATASIIGDVMGPTLNNLNNLURLSPGC 1186
922 GEQNNIFAPNIYILDYLTKKKQLTDNLKELKALSMRQGYQRELLYQREDFGSFAFNVD 981
1187 GEQNNIFAPNVFVLKYLQTKQQLSPVERETDYLQGYQRLTYRQDGSYAFGERD 1246
982 PSGSTWLSAFVLRCPLEADPYIDIDQNLHRTYTWLKGHOKSNGEFWDPRGVHSELOGG 1041
1247 ASGSMLTAFVLSKFAQARSEFVDPRELAASKWIIQQOQADGSLAVGRVNLKNDIOGG 1306
1042 NKSPVTLTAYITVTSIL--GYRKYQPNIDVQESIHFLESEFSRGISDNVTALITAYALSIV 1099
1307 IHGIVPLTAYVVVALLETGTASEERSTDKARHFLSESAAPLAM-DPYSICALITYALTLL 1365
1100 GSPKAKEALNMLTWRAEQEGMQFVWSSESLSQSWQPR-----SLDIE 1143
1366 RSPAPEALRKLRSILAIMRDCGVTHW-----SLNSWDVDKGTFLSFDVSVSVAEVE 1420
1144 VAAVALLSHFLQFQTSCEGIPIMRWLSRCNSLGGFASTQDITVALKALSEPAAL----- 1197
1421 MTAVALLTYLLGDVAAALPVVKWLSQQRNALGGFSSQDTCVALQALAEVAILYSAGGI 1480
1198 -----MNTERTNIQVTVTG--PSPSPSLAVVQPMVNI SANGFGFAICQ 1239
1481 NLTVSLASTNLDYQTFELHRTNOKVLQTAAPSLTGLFV-----APDLVAVKENK 1274
1240 LNVTVNVK--ASGSSRRRRSIQOE----- 1532
1533 IDVTVPDPVAKFAFQLLVLSLOPFAQGRPPMPASAAEGSRGDWPPADDDPAADQHH 1592
1275 DDLNHDVNVCTSTSGPGRSGMALMEVNLISGFMVPSFAISLSST-----VKKVEYDH 1327
1593 QEYK--VMEVETRWLHAGSSNMAVLEVPLLSGFRADIE--SLEQLLLDKEMGMKRYEVAG 1649
1328 GKLNLYLDSV-NEQFCVNIAPVNFKNVNTQDASVIVDYIEPRQAVRSYSEV----- 1382
1650 RVLVYFDEIPSRCLTCVFRALRECVVGRTSALPVSYDYIEPAFAFATRYNVNTHSPL 1709
1393 --KSSCDLCSDVQ-----GCRPCEDGSGSHHSSVI 1413
1710 ARELCAGPACNEVERAPARGCFWPFPGSGPAPAVEEGNAI 1749

RESULT 10

US-09-972-211-69

Sequence 69, Application US/09972211

Publication No. US20040048245A1

GENERAL INFORMATION:

APPLICANT: Shimkets, Richard A

APPLICANT: Taupier Jr, Raymond J

APPLICANT: Burgess, Catherine E

APPLICANT: Zerhusen, Bryan D

APPLICANT: Mezes, Peter S

APPLICANT: Rastelli, Luca

APPLICANT: Malyankar, Uriel M

APPLICANT: Grosse, William M

APPLICANT: Alsobrook II, John P

APPLICANT: Lepley, Denise M

APPLICANT: Spytek, Kimberly Ann

APPLICANT: Li, Li

APPLICANT: Edinger, Shlomit

APPLICANT: Gerlach, Valerie

APPLICANT: Ellerman, Karen

APPLICANT: MacDougall, John R

APPLICANT: Gunther, Erik

APPLICANT: Millet, Isabelle

APPLICANT: Stone, David J

APPLICANT: Smithson, Glenda

APPLICANT: Szekeres Jr, Edward S

TITLE OF INVENTION: No. US20040048245A1 Human Proteins, Polynucleotides Encoding The

TITLE OF INVENTION: Methods Of Using The Same

FILE REFERENCE: 21402-141

```

; CURRENT APPLICATION NUMBER: US/09/972,211
; CURRENT FILING DATE: 2001-10-05
; PRIOR APPLICATION NUMBER: 60/238,325
; PRIOR FILING DATE: 2000-10-05
; PRIOR APPLICATION NUMBER: 60/238,323
; PRIOR FILING DATE: 2000-10-05
; PRIOR APPLICATION NUMBER: 60/238,400
; PRIOR FILING DATE: 2000-10-06
; PRIOR APPLICATION NUMBER: 60/238,397
; PRIOR FILING DATE: 2000-10-06
; PRIOR APPLICATION NUMBER: 60/238,401
; PRIOR FILING DATE: 2000-10-06
; PRIOR APPLICATION NUMBER: 60/238,379
; PRIOR FILING DATE: 2000-10-06
; PRIOR APPLICATION NUMBER: 60/238,402
; PRIOR FILING DATE: 2000-10-06
; PRIOR APPLICATION NUMBER: 30/238,384
; PRIOR FILING DATE: 2000-10-06
; PRIOR APPLICATION NUMBER: 60/238,373
; PRIOR FILING DATE: 2000-10-06
; PRIOR APPLICATION NUMBER: 60/238,372
; PRIOR FILING DATE: 2000-10-06
; PRIOR APPLICATION NUMBER: 60/238,383
; PRIOR FILING DATE: 2000-10-06
; PRIOR APPLICATION NUMBER: 60/238,382
; PRIOR FILING DATE: 2000-10-06
; PRIOR APPLICATION NUMBER: 60/275,892
; PRIOR FILING DATE: 2001-03-14
; PRIOR APPLICATION NUMBER: 60/296,860
; PRIOR FILING DATE: 2001-06-08
; NUMBER OF SEQ ID NOS: 198
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 69
; LENGTH: 1476
; TYPE: PR1
; ORGANISM: Cavia porcellus
; US-09-972-211-69

Query Match      20.3%; Score 1491; DB 12; Length 1476;
Best Local Similarity 28.8%; Pred. No. 1.le-112;
Matches 451; Conservative 292; Mismatches 524; Indels 300; Gaps 60;

QY 4 PPLTAAHLVCVTAALAVAPGRFLVATGPIRPGNVTVIGVELLEHCPQVTVKAEI- 62
Db 11 PVLL-----LLILLAADASISGQYMYLVPSLSEGTPEKICL-LTLQNLNETVTKASLD 65
QY 63 -LKTASNLTVLEAEQVPEKGFKTLTLPSLPLNSADEIYELRVGTQDEILFNSR 121
Db 66 TIRENGSLFNMVAEKDLFOCVAF---TVQSPYPEAVMFLTVVEGPTHG---FRSRKT 119
QY 122 LSFETKRISVFIQTDKALYKQKQVPRVITLPSDFPKPKYKTSLN-----ILIKDPKSNLI 176
Db 120 VLKSKDSLVEVQTDKPIYKPGQTVKARVVSLDENFRP-----LNELPFLIFIQDPKGNRV 175
QY 177 QWLISOQSDLGVLISKVTFOLSSHPIILGDWSIQV-QVNDQTYQSFQVSEVULPKFEVTLQT 235
Db 176 MOWNLKLERGLTQLSFPPLSEPLLSYSVVVHKGSGRHHHSFTVEEFVLPKPEVQVSM 235
QY 236 PLVCSNMSKHLNGTITAKYTYGPKVGDVTLTEL-----PLSFWKKKNIITKF---KING 288
Db 236 PKXITILEQEFYVSGRYTYGKVPNGNITMSICRNVNPSACLSE---SRAFCCKYQ 292
QY 289 SAN-----FNFDEEMK-----NMDSSNGLSEYLDLSPGPVEILTTVT 328
Db 293 QLNSQCGFICQVKTNDPFLRKEVEMLRVEAKIREEGTG---VQLTGTGFSEITATIT 348
QY 329 ESVTGISRNVTNVFFKQHDYIIEFFDYTVLAKPSLNFTATVKVTRADGNQLTLEERRNN 388
Db 349 K-----LSFVKVDSYVRPGVFFPGQVRL--VDCGNVMPHMK--- 383
QY 389 VVITVQRNTEYWSGNSGNQRMEAVQ-KINTVTPQSGTFKIEFFILEDSS-----ELQ 443
Db 384 ITITASEANY-----HSNATTDEGLVQFSINTNMIGTSLNIQVXKHDSTNCYDQWLL 438

444 KAYFLGSKSSMAVHSLFKSPSKTYIQLKT-----RDENIKVGSPPELVVSGNKRKE 495
439 EANEAGASHANAVFSL-----SRSFVHLEPQLGKLPCHQOTQTFKA---HYILKG-QELKE 489
496 L--SYMVVSRGQLVAVG-----KONST-----MMSLTPENSWTPKACVIVVYIEDGGII 543
490 LVFYVIMAKGGIVOSGTYVLSVEQNTKGHFSVSPVESDLAPVARVLIITAILPSGII 549
544 SDVLKIPVQLVPKNIKLYMSKVAABSEKVSLSAISVTPQDSIVGIVAVDSKVNLI----- 598
550 ADSAKYNVENCIDKNVLSFSEGQSLPASKTHLRVTAS-POSICALRAVDQSVLLRKEPA 608
599 -MNASN-----DIT-----MENVVHELELYNTGYLGMF-----MNSFA 631
609 VLSASSVYALLPVKDLTGFPGLLGOQENDEGECVSLYNT-YIDGLYSPENINEKMYG 667
632 VFQECGLWLTDANLT KDYIDGVVDNARYAERFMEENEHGHIVDIDHDFSLGSSPH----- 685
668 FLKDMGLKVFNTKIQKPOLCAHVQKFEVPTMAYSSSESS-----SFRSGPRRPAVG 720
686 -----VRKHFPETWIW---LDTNMGYRIYQEFVTVPPDSITSWATGVI SED 730
721 IAAATYSEPPKETVRYSEETWMDLKVTDSSG---VAEVEVTVPTITENKAGAFCLSD 777
731 LGLGLTTTPVELQAFQPPFIFLNLPSYVIRGEFALEITINYLKDAVEVKVIEKSKDF 790
778 TGLGLSPT-ASLRAPQPEFVELTMPYSVIRGEAFTLKATVNLVLPDCIRISVHLEASPKF 836
791 DILMTSSEINATGHQOTLLVPSEDAATVLPFIRPHLGEIPITVTA----- 836
837 LAEPKAKE-----QESYCVCGNERQTVSWVTPKSLGNVNFVSAELESSELGNEKT 890
837 LSPT--ASDAVTOMLLVKAEGIEKYSQSILDLTDNRLOSTLKTLSFSPFNPVTGSE 894
891 VVPTPKKDTTIKPLLEVPFEGLEKEETWTSIRVSDTTVS---EKHLELSNVTQDSAR 947
895 VOITAIGDVLGPSINGLASLRMPYGCGEQNMIFAPNIYIIDLTKKKQLTDLNKEAL 954
948 ATVSILGDILGSAMQNIQLQMPYGCGEQNMVLPAPNIYVLDVLYNETQOLTPODKSKAI 1007
955 SFMRQGYORELLYQEDQSFSAFG-NY-DPSGSTWLSAFVLCRLEADPYDIDQNVLR 1012
1008 SYLSTGYQRQNYHRDGSYSTFGNRYGOGNWTMTAFVLKTFQSARKYFIDEAHTQ 1067
1013 TYTWLKGHKQNGEFPDGRVHSHSLOGNKSPTVLTAYIVTSLIGYKQYQNTDQBSI 1072
1068 ALSWLSQKQKNGCFWSSGSLNNAIKGVEDELSLSAYITIALLEMSLPDTHPVVRNAL 1127
1073 HFLES-----EFSRGISDNTYLAITVALSSVGS-PKAKEALNMLTWRAEQEGMQPWV 1125
1128 FCLESAMKSAKEGTHG-SHVYTKALLAYAFALAGNQERKEILKSLEDEGVKEDNSLHWA 1186
1126 SSES-KLSDSW---QPSLDIEVAAYALLSHFLQFOTSEGIP-----IMRWLSR 1170
1187 RPQKPKVSEGFLPKSQAPSAEVMTSYVLLAYL---TARPAPTEDUTSATDINNVYIK 1242
1171 QRNSLGGFASTQDITVALKALSEFAA---LMNTERNTIQVTVTPSSPSP-----LAV 1220
1243 QQNSHGGYSSQDITVALHALSKYAAATFTRTERKA-AQVTIKSSGCTPTNFEVANNHLL 1301
1221 VQPMAY-----NISANGFGAICOLNVVNV-----KASGSSRRR 1256
1302 LQQVSLPTVSDSYTITVTGEGNVYLOSLKYNVPSSEKGTFFPFALEAETVPOACGPKAHT 1361
1257 STQNEAFDLVDVAVKENKDDLNVLDLVNCTSFSGRSGMALMEVNLISGF--MVPS-EA 1313
1362 SFQ-----ISLNVSYIGSRP-VSNMAIVDKVMSGIFPLKPTVK 1400
1314 ISLSTVKKVYDGHKLNLYLDSVNETQFCVNIIPAVRNFKVSNTOQDASVSVIYDYEPRRQ 1373
1401 LEKSEHSIRTEVSNHVLIIYLDKSVNQTSLSFFVQDIEVRDLKPAIKYDYIYETNEF 1460
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Qy 1374 AVRSYNS 1380
Db 1461 AIAEYHA 1467

US-10-096-625-69
Query Match 20.3%; Score 1491; DB 12; Length 1476;
Best Local Similarity 28.8%; Pred. No. 1.1e-112;
Matches 451; Conservative 292; Mismatches 524; Indels 300; Gaps 60;

RESULT 11
US-10-096-625-69
Sequence 69, Application US/10096625
Publication No. US20040068095A1
GENERAL INFORMATION:
APPLICANT: Shinkets, Richard A
APPLICANT: Taupier Jr, Raymond J
APPLICANT: Burgess, Catherine E
APPLICANT: Zerhusen, Bryan D
APPLICANT: Mezes, Peter S
APPLICANT: Rastelli, Luca
APPLICANT: Malyankar, Uriel M
APPLICANT: Grosse, William M
APPLICANT: Alsobrook II, John P
APPLICANT: Lepley, Denise M
APPLICANT: Spytek, Kimberly Ann
APPLICANT: Li, Li
APPLICANT: Edinger, Shlomit
APPLICANT: Gerlach, Valerie
APPLICANT: Ellerman, Karen
APPLICANT: MacDougall, John R
APPLICANT: Gunther, Erik
APPLICANT: Millet, Isabelle
APPLICANT: Stone, David J
APPLICANT: Smithson, Glenda
APPLICANT: Szekeres Jr, Edward S
APPLICANT: Ji, Weizhen

TITLE OF INVENTION: No. US20040068095A1el Human Proteins, Polynucleotides Encoding Th
TITLE OF INVENTION: Methods Of Using The Same
FILE REFERENCE: 21402-141 CIP
CURRENT APPLICATION NUMBER: US/10/096,625
CURRENT FILING DATE: 2002-03-13
PRIOR APPLICATION NUMBER: 09/972,211
PRIOR FILING DATE: 2001-10-05
PRIOR APPLICATION NUMBER: 60/238,325
PRIOR FILING DATE: 2000-10-05
PRIOR APPLICATION NUMBER: 60/238,323
PRIOR FILING DATE: 2000-10-05
PRIOR APPLICATION NUMBER: 60/238,400
PRIOR FILING DATE: 2000-10-06
PRIOR APPLICATION NUMBER: 60/238,397
PRIOR FILING DATE: 2000-10-06
PRIOR APPLICATION NUMBER: 60/238,401
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PRIOR APPLICATION NUMBER: 60/238,383
PRIOR FILING DATE: 2000-10-06
PRIOR APPLICATION NUMBER: 60/238,382
PRIOR FILING DATE: 2000-10-06
PRIOR APPLICATION NUMBER: 60/275,892
PRIOR FILING DATE: 2001-03-14
PRIOR APPLICATION NUMBER: 60/296,860
PRIOR FILING DATE: 2001-06-08
NUMBER OF SEQ ID NOS: 200
SOFTWARE: PatentIn ver. 2.1
SEQ ID NO 69
LENGTH: 1476
TYPE: PRT
ORGANISM: Cavia porcellus

US-10-096-625-69
Query Match 20.3%; Score 1491; DB 12; Length 1476;
Best Local Similarity 28.8%; Pred. No. 1.1e-112;
Matches 451; Conservative 292; Mismatches 524; Indels 300; Gaps 60;

Qy 4 PPLTAHLLCVCTAALAVAPPRFLYTAFCIIIRPGGNVTIGVELLHCHSFOVTVKAEI- 62
Db 11 FVLL-----LLLLAADASISGKQPMVLVPSLLHSGTPEKICL-LLTQLNETVTVKASLD 65
Qy 63 -LKTASNLTVSVAEGVFEKGSFKTLTLPSPILNSADEIYELRVGTGRTODELFSNSTR 121
Db 66 TIRENGSLFMMVAEKOLFQCVAF---TVQSPYPEAMVFLTVEGPTHG---FRSRKT 119
Qy 122 LSFETKRISVFIOTDKALYKPKQEVKFRIVTLPSDFPKYKTSLN-----LLIKDPKSNLI 176
Db 120 VLVKSKDSLAVFQTDKPIYKPGQTVKARVSLDENFRP-----LNELPFLIFIQDPKGNRV 175
Qy 177 QOWLSQQSDLGVISKTFQLSHPILGDWSIOV-QVNDQTVYQSFQSVYVLPKPEVTLQT 235
Db 176 MQWQNLKLERGLTQLSPLESPELGSYVVVHKESGGRMHHSFTVEFVLPKREVQVSM 235
Qy 236 FLYCSMNSKHLNGITITAKYTYGKPVKGDVTLTFL-----PLSPFGKKKNITKTF--KING 289
Db 236 PKKITILEQETVSVCGRYTYGKVPVGNITMSICRNYNPNPSACLSEE---SRPFCKYINQ 292
Qy 289 SAN-----FSFNDSEMK-----NWDSSNGLSEYLDLSSGCPVEILTTVT 328
Db 293 QLNQGGCFIOQVKTNDPQLRREKYEMLRVEAKIREGTG-----VQUTGTGFSBITAIT 348
Qy 329 ESVTGISRNVTNVFFKQHDYIIIEFFDYTTVLKPSLNFATVKTVRADGNQLTLLEERNN 388
Db 349 K-----LSFVKDVSIVRPGVPFGQVRL--VDGNVMPHXM-- 383
Qy 389 VVITVQRNYTEYWSGNSGNQKQEAQV-KINYTVPOSQTKIEFPPILESS-----ELQL 443
Db 384 ITITASEANY-----HGNATTDENGLVQFSINTNMIGTSLNQVHKHDSCTNVDYQWLL 438
Qy 444 KAYFLGSKSSMAVHSLPKSPSKTYIQLKT-----RDENIKVGSPPFELAVVSNKELKE 495
Db 439 EANECASTANAVESL-----SRSFVHLEPQLGKLPCHQQTQTFKA---HYLKG-QELKE 489
Qy 496 L--SYMVSRGOLVAVG-----KQNST-----MPSLTPENSWTPKACVIVYIIBDDGEII 543
Db 490 LVFYVYVIMAKGGIVQSGTYVLSVEQNTKGHFSVPVESDLAEFVARVLIYALPSGEII 549
Qy 544 SDVLKIPVQLVFKNKIKLYWSKVAEPSEKVSLSRISVTPQDSIVGIVAVDKSVNL----- 598
Db 550 ADSAKYVENCIDNKNVLSFSEGSLPASKTHLRVTAS-POSICALRAVDQSULLRKEPA 608
Qy 599 -MNASN-----DIT-----MENVVHELELYNTGYLQNF-----MNSFA 631
Db 609 VLSASSVYALLPVKDLTGFGLLGQOEENDGECVSLYNT-YIDGILYSPENINEKDMYG 667
Qy 632 VFOECQLWLTDLNLTXDYIDGVYDNAEYAFRFEENECHIVDHDPSLSSPH----- 685
Db 668 FLKQMLGLVFTNTKIQKQPCALHVKQKFEVPTMAYSYESS-----SFGSPRRVPAVG 720
Qy 686 -----VRKHPPETMIW---LDTNNGYRIYQEFVTVPSDTSITSWATGFVISED 730
Db 721 IAAATYSEPPKETVRTYSPETWIDLKVTDSSG---VAEVEVTVPTITTEWKAGAFCLSD 777
Qy 731 LGLGLTTPVLOLQAPPPFIPLNLPYSVIRGEEFALITIFNYLKDATEVNIIEKSKDF 790
Db 778 TGLGLSPT-ASLRAFQPPFVELTWPYSVIRGEAPTTLKATVNLVLPDCIRISVHLEASPKF 836
Qy 791 DILMTSSSEINATGHQOULLVPSEDCATVLPPIRTHLGEIPIVTA----- 836
Db 837 LAEPKAKE-----QESYCVCGNERQTVSWVTPKSLGNVNTVSABALESELCEGNEKT 890
Qy 837 LSPT--ASDAVTOMILVKAEGIEKSYQSILDLTDNRLOSTLTKTSLFSFPNTVTSER 894
Db 891 VVPTYGKXDTIIPKLLVEPEGIEKEETWTSLRVSDTTVS---EKLHLELPNSVNIQDSAR 947


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Db      442 EEAHTAY-----LVFSPKSFVHLEPMGHELPCHGTQTQVQARYILNGGTLG 489
QY      493 LKELS--YMWVSRGOLVAVG-----KONST-----MFLTPENSWTPKACVIVYVIEDDG 540
Db      490 LKLSFYILMAKGGIVRTGTHLLVKQEDMKGHFSISIPVKSADIAPVARLLIYAVLPTG 549
QY      541 EIIISDLKIPVQLVFKMKILYKSKVKAEPSEKVSIRISVTPQDSIVGIVAVDXSNILM- 599
Db      550 DVIQDSAKYDVENCLANKVDLSFSPSQSLPASHAHLRVTA--PQSVCALRAVDQSVLLMK 608
QY      600 -----NAS-----NDITMNVVHELELYNTGY-VLGMFNMS-----FA 631
Db      609 PDAELSSASVNLPEKDLTGFGPLPDQNDQNCIIRHNHYINGIITYTPVSSTNEKDMYS 668
QY      632 VFQECGLWLTDLNLTROYIDGVYDNAE-----YAEFMBENEGHIVDIDHPSL 680
Db      669 FLEDMGLKFTNSKIRPKMKPCPOLQOYEMHGPGLRVGFYSDVMGKGHARLVHVEE--- 725
QY      681 GSSPH---VRKHPPETHWIDTMGYRIYQBFVTVTPDSITTSWVATGFVISEDGLGLTT 737
Db      726 ---PHTETVKYFPETWDLVNVNSAGVAEVTVPDITTEWKAGAPCLSEDAAGLIS 782
QY      738 TPVELQAFQFFPIPLNYPYVIRGESEFALBITITFNLYKDATEVKVIEKSKDFDILMTSS 797
Db      783 T-ASLRAFQFFVELTWPYVIRGEAFTLKATLVNLPKIRVSVQLEASPAFLAVPVEK 841
QY      798 E-----INATGHQOTLLVPSEDAATVFPPIRPHLGEIPITVIALS-----PTA 841
Db      842 EQAPHICICANGRQ-----TVSWAVTPKSLGNVNFVTSAALESQELCGTEVPVS 890
QY      842 -----SDAVTQMIILVKAEGIEKYSQSILDLTDNRLOSLTKLTSFSPPTVTGSEYQ 896
Db      891 PEHGRKDTVTKPLLEPEGELEKETTNSLLCPGGEVS---EELSXLPPNVVESEARAS 947
QY      897 ITAIGDVLGSPINGLASLIRMPYCGGQNNMINFAPNIYDLYTKKKQKLTDLNKEALSF 956
Db      948 VSVGLDILSAMQNTQNLQMPYCGGQNNVLEAPNIYVLDYLNETQOLTPEIKSKAIGY 1007
QY      957 MRQGYQRELYIQREDDGSFSAFG-NYDPS-CSTWLSAFVLCFLEADPYDIDQNVLHRY 1014
Db      1008 LNTGYQRLNKKYHVDGYSYSGERYGNQNTWLTAPVLKTFQAARAYIFIDBAHITQAL 1067
QY      1015 TWLKGHQSNGEFWDPCRVIHSELQGNKSPVITITAYIVTSLGYSKYQFNIDVQSEIH 1074
Db      1068 IWLQKQKNGCFRSGSLNNAIKGGEDEVLSAVITIALLEIPLTVTHPVVRKALFC 1127
QY      1075 LES-----EFSRGISDNYITALITYALSSVGS-PKAKEALNMLTWRAQEGGMQFW--- 1124
Db      1128 LESAWKTAQEGDHG-SHYVYTKALLAYAFALAGNODKRKEVYKLSNEEAVKKNVSHWRSP 1186
QY      1125 VSSEKLSDSWQPR--SLDTEVAAYALLSHFLOFQ---TSEGIP---IMRMLSRORNSL 1175
Db      1187 QXKAPVGHYEFQAPSAEVMYSYVLLA-YLTAQAPATSEDLTSATNIVKWTQKQNAQ 1245
QY      1176 GGFASDTQTTVALKALSEFALNMTERNTQVTVTPSPSPPLAVQ----- 1222
Db      1246 GGFSSDTQTTVALHALSKYGAATFT-RTGKAAQVTTQSSGTFSSKFTQVNNRLLLQOVS 1304
QY      1223 -----PMAVNISANGFPAICQLAVNVYVNVKAGSSRRRRSIQNGEAPDLDVAVK---ENK 1275
Db      1305 LPELPGYSMKVTGEGCVYIQLTSKYN-----LPEKEEPPFALGVOTLPTQCD 1353
QY      1276 DLN-HVDLVNCTFSGPG---RSCMALMEVNLISGFVMPSEAI SL---SETVKVEYDHG 1328
Db      1354 EPKXHTSFQISLSVSYGSRASANAIVDVKWSGFIPLKPTVKMLERSNHVSRTVSSN 1413
QY      1329 KXNLVDSVNETQFCVNIPAVRNFKVSNTQDASVSIVDVYEPFRQAVRSYNS 1380
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US-10-096-625-65
; Sequence 65, Application US/10096625
; Publication No. US20040068095A1
; GENERAL INFORMATION:
; APPLICANT: Shimkets, Richard A
; APPLICANT: Taupier Jr, Raymond J
; APPLICANT: Burgess, Catherine E
; APPLICANT: Zernusen, Bryan D
; APPLICANT: Mezes, Peter S
; APPLICANT: Rastelli, Luca
; APPLICANT: Malyankar, Uriel M
; APPLICANT: Grosse, William M
; APPLICANT: Alsbrook II, John P
; APPLICANT: Lepley, Denise M
; APPLICANT: Spytek, Kimberly Ann
; APPLICANT: Li, Li
; APPLICANT: Edinger, Shlomit
; APPLICANT: Gerlach, Valerie
; APPLICANT: Ellerman, Karen
; APPLICANT: MacDougall, John R
; APPLICANT: Gunther, Erik
; APPLICANT: Millet, Isabelle
; APPLICANT: Stone, David J
; APPLICANT: Smithson, Glenda
; APPLICANT: Szekeres Jr, Edward S
; APPLICANT: Ji, Weizhen
; TITLE OF INVENTION: No. US20040068095A1el Human Proteins, Polynucleotides Encoding The
; FILE REFERENCE: 21402-141 CIP
; CURRENT APPLICATION NUMBER: US/10/096,625
; PRIOR FILING DATE: 2002-03-13
; PRIOR APPLICATION NUMBER: 09/972,211
; PRIOR FILING DATE: 2001-10-05
; PRIOR APPLICATION NUMBER: 60/238,325
; PRIOR FILING DATE: 2000-10-05
; PRIOR APPLICATION NUMBER: 60/238,323
; PRIOR FILING DATE: 2000-10-05
; PRIOR APPLICATION NUMBER: 60/238,400
; PRIOR FILING DATE: 2000-10-06
; PRIOR APPLICATION NUMBER: 60/238,397
; PRIOR FILING DATE: 2000-10-06
; PRIOR APPLICATION NUMBER: 60/238,401
; PRIOR FILING DATE: 2000-10-06
; PRIOR APPLICATION NUMBER: 60/238,379
; PRIOR FILING DATE: 2000-10-06
; PRIOR APPLICATION NUMBER: 60/238,402
; PRIOR FILING DATE: 2000-10-06
; PRIOR APPLICATION NUMBER: 30/238,384
; PRIOR FILING DATE: 2000-10-06
; PRIOR APPLICATION NUMBER: 60/238,373
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; PRIOR FILING DATE: 2000-10-06
; PRIOR APPLICATION NUMBER: 60/238,382
; PRIOR FILING DATE: 2000-10-06
; PRIOR APPLICATION NUMBER: 60/275,892
; PRIOR FILING DATE: 2001-03-14
; PRIOR APPLICATION NUMBER: 60/296,860
; PRIOR FILING DATE: 2001-06-08
; NUMBER OF SEQ ID NOS: 200
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 65
; LENGTH: 1474
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-096-625-65
Query Match 19.6%; Score 1441; DB 12; Length 1474;
Best Local Similarity 29.2%; Pred. No. 1.5e-106;
Matches 453; Conservative 264; Mismatches 551; Indels 284; Gaps 60;
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Db 125 EDSLIVFQTDKSIYKPGQTVKFRVSMNDENFHPNLNLIPLVYIQDPKGNRIQWQSFQLE 184
Qy 186 LGVISTKTFQSSHPILGDNISIQVQND--QTYYSQSFQSEYVLPKFEVTLQTPLYCSMNS 243
Db 185 GGLKQSFPLSSBPFQSGYKVVVQKSGGRTEH-PFTVEFVLKPEVQVTPKIIITILE 243
Qy 244 KHLNGTITAKYTKGPKVKGVDVTLFPL-----SFWGK 276
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Qy 277 KGNITKFKINGANFENDEEMKNVMSNGLSSEYLDLSSPGVRLT-----TFTESV 331
Db 304 VK--TKVPQLK-----KEYEK-----LHTEAQIOEGTVVVELTGROSSEITRI 347
Qy 332 TGISRNVTNVFKQHDYIIEFPDYTVLKPNSLNFATVKTADGNQTLERNNVVI 391
Db 348 TKLS-FVKVDSPHQ--IPFFG-----QVRLVDGKGVPIP-----NKVI 384
Qy 392 TVTORNVTYWSGNSGNQKWEAVO-KINYT--VPOSGTFKIEFP-----LLEDS 438
Db 385 FI-RCNEANY--SNATDDEGLVQPSINTVMTSLTVRVNYKDRSPCYGQWVSEB 441
Qy 439 SELOLKAYFLGSKSSMAVHSLFSPSKTYIQLTRDENIKVGS-----PPELVVSGNK--R 492
Db 442 EEAHTAY-----LVSPSKSFVHLEPMSHELPCGHTQTVOAHVILNGGTLG 489
Qy 493 LKELS--YMVVSRGOLVAG-----KONST-----MPSLTPENSWTPKACVIVYIEDG 540
Db 490 LKLSFYLLINAKGIVRTGHLVLLKQEDMKGHFSISIPVKSDIAPVARLLIYVLP 549
Qy 541 EISDVLKIPVLVFNKIKLYSKVKAEPSEKVSIRISVTPQDSVIGVAVDQSNLNM- 599
Db 550 DVIGDSAKYDVENCLANKVDLSFSPQSPLASHAHLRVTA--PQSCALRAVDQSVLLMK 608
Qy 600 -----NAS-----NDITMNVVHELELYNTGY-YLGNFMS-----FA 631
Db 609 PDAELSSAVYNLLPEKDLTGFPGLDQDNDQNCINRHNHYINGITYTVPVSTNEKDMYS 668
Qy 632 VFDEGLWLTDLNLTVDYIDGVYDNE-----YAEFMEENECHIYDIHDFSL 680
Db 669 FLEDMGLKATNSKIRKPKMCPQLQYEMHGPGLRVGFVESDVNGRGHARLVHVEE--- 725
Qy 681 GSSPH-----VRKHFPETWIDTNGVRIYQEFVTVPDSTISWVAQFVISEDGLGLTT 737
Db 726 ---PHTETVRKYPETWIDLVVNVNAGVAEUGVTPDITTEWKAGAFCLSEDAGLIGSS 782
Qy 738 TPVELQAFQFFIFLNLPIVIRGEPEALBITFNYLKQATEVKVILEKSKDFDILMTSS 797
Db 783 T-ASLRAFQFFVELTNPYVIRGEATPLKATVNLVLPKIRVSVQLEASPAFLAVPEK 841
Qy 798 E-----INATGHQOQLLVPSEGDATVFPPIRTHLGEPIITVTLAS-----PTA 841
Db 842 EQAFHCICANGRQ-----TVSWAVTPKSLGNVFTVSAEALQSQELCGTEVPSV 890
Qy 842 -----SDAVTQMLVIAEGIEKYSQSIIILDLDNRLOSTLKLTSFPFPNTVGSERVQ 896
Db 891 PEHGRKDVTKPLLAVEPEGELEKETTFFNSLLCPGSGEVS---EELSUKLPNVVVEESARAS 947
Qy 897 ITAIGDVLGPSINGLASLRMPYCGGQNNMINFAPNIYIIDLTKKQLTDLNLEKALSF 956
Db 948 VSVLGDILGSAMQNTQLLQMPYCGGQNNVLPAPNIYVLDYLNETQQLTPEIKSAIGV 1007
Qy 957 MRQYQRELYQREDSGFSAG-NYDPS-GSTWLSAFVLCFLEADPYDIDQVLRHY 1014
Db 1008 LNTGYQRLNKKYDYSYSTFGERYGNQNTWLTAFVLTFAQARAYFIDEAHTQAL 1067
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Db 1068 IWSQRQDNGCCFRSSOSILNNAIKGVEDEVILSAITIALLEIPLVTHPVVRNALFC 1127
Qy 1075 LES-----EFSRGISDNYTIALITYALSNGS-PKAKEANMLTWRABQEGMGQW--- 1124
Db 1128 LESAWKTAQEGDHG-SHYVTKALLIAYAFALAGNQDKRKEVLKSLNEBAVKONSVHWERP 1186

Qy 1125 VSSSKLSDSQPR--SLDIEVAAAYALLSHFLQFQ---TSEGIP-----IMRWLSRQNSL 1175
Db 1187 OKPAPVGHFYEPOQAEVEMTSYVILLA-YLTAQAPAPTSEDLTSAITNIVKWTQQNAQ 1245
Qy 1176 GGFASDTODTTVALKALSEFAALMNTERTNIQVTVTGSSPSPLAVQ----- 1222
Db 1246 GGFSTQDVTVALALSKYGAATF-RTGKAAQVTIQSSGTFSSKFQVDNNRLLLOQS 1304
Qy 1223 ----PMAYISANGFGFAICQANVYVYKASGRRRRSQRONQAFDLDVAVK---ENKD 1275
Db 1305 LPELPGEYSMKVTEGECVYLQTSKXNI-----LPEKEEFPFALGVQTLPTOTCD 1353
Qy 1276 DLN-HVDLNVCTSSGPG---RSGMALMEVNLLSGFVMPSEBAIL--SETVKKVEYDHG 1328
Db 1354 EPKAHTSFQISLSVSYTGSRSASNAIVDVQWMSGFPLKPTVKMLERSNHVSRTEVSSN 1413
Qy 1329 KINLYLDSVNETQFCVNIAPVRNFKVSNTOQASVSIYDVEYPRRQAVRSYNS 1380
Db 1414 HVLIVLDKVSNTLSLFTVLQDVPVRDLKPAIVKVYDYETDEFAIAEYNA 1465

RESULT 15

US-10-052-817-2
; Sequence 2, Application US/10052817
; Publication No. US20020114792A1
; GENERAL INFORMATION:
; APPLICANT: Tanzi, Rudolph E.
; APPLICANT: Kovacs, Dora
; APPLICANT: Saunders, Aileister J.
; TITLE OF INVENTION: Alpha-2-Macroglobulin Therapies and Drug Screening Methods for
; TITLE OF INVENTION: Alzheimer's Disease
; FILE REFERENCE: 0609.4460005
; CURRENT APPLICATION NUMBER: US/10/052.817
; CURRENT FILING DATE: 2002-01-23
; PRIOR APPLICATION NUMBER: 09/241,606
; PRIOR FILING DATE: 1999-02-02
; PRIOR APPLICATION NUMBER: 09/148,503
; PRIOR FILING DATE: 1998-09-04
; PRIOR APPLICATION NUMBER: 60/093,297
; PRIOR FILING DATE: 1998-07-17
; NUMBER OF SEQ ID NOS: 27
; SOFTWARE: Patent in Ver. 2.0
; SEQ ID NO 2
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-052-817-2

Query Match 19.6%; Score 1441; DB 13; Length 1474;
Best Local Similarity 29.1%; Pred. No. 1.5e-108;
Matches 451; Conservative 266; Mismatches 551; Indels 284; Gaps 59;

Qy 12 LLCVCTAALAVAPGPRFLVTAAGIIRPGNVITIGVELLEHCPQSVTVKAEILLKTSNLTV 71
Db 15 LLVLPTDASVSGPQYVNLVPLSLHT-ETTEKCVLLSYLNETVTVSASLESVGRNSL 73
Qy 72 -SVLEAEG-VFEKSGFKTLPLSPILMSAD-YYELRVGTQDRLSNTRLSFET 126
Db 74 FTDLEAENDVLHCAF-----AVPKSSNEEVNFLTQVKGPTQE---FKRITVAVKN 124
Qy 127 KRISVFIOTDICALYKQEVKFRIVTLFSDFKPKYKTSNLIL-IKDPKSNLIQWLSSQSD 185
Db 125 EDLSLVFVOTDLSIKYKPGTVKFRVVMNDENFHPNLNLIPLVYIQDPKGNRIQWQSFQLE 184
Qy 186 LGVISTKTFQSSHPILGDNISIQVQND--QTYYSQSFQSEYVLPKFEVTLQTPLYCSMNS 243
Db 185 GGLKQSFPLSSBPFQSGYKVVVQKSGGRTEH-PFTVEFVLKPEVQVTPKIIITILE 243
Qy 244 KHLNGTITAKYTKGPKVKGVDVTLFPL-----SFWGK 276
Db 244 EEMNVSVGLTYTGKVPVGHVTVSICRKYSDASDCHGEDSQAFCEKFSQOLNSHGCFYQO 303

QY 277 KNIITKTFKINGSANFENDEEMKVNVDSSNGLSLEYLDLSSPGPVELT-----TWTESV 331
Db 304 VK-TKVFOUKR-----KEYEMK-----LHTEAQIOEBGTIVVELTGRQSEITRII 347
QY 332 TGSRNVTNVFPKQHDYIIIEFFDYTTVLKPSLNFATVKTTRADGNQLTLEERRNVVI 391
Db 348 TKLS-FVKVDSHFRQG---IPFEG-----QVRLVDGKGVPPI-----NKVI 384
QY 392 TVTORNTEYKSGSNGQKWEAVO-KINYT--VPOSGTFKIEFP-----LLEDS 438
Db 385 FI-KGNEANYI--SNATTDHGLVQPSINTNVKGTSLTVRVNKKORSPOCYGYQWVSEEH 441
QY 439 SEIQLKAYFLGSKSSMAVHSLFKSPSKTYIQLTRDENIKVGS----PFEVLVSGNK--R 492
Db 442 EEAHTAY-----LVFSPSKSFVLEBPMSEHPCGHTQTQVAHYILNGGTLG 489
QY 493 LKELS--YMTVSRQOLVAVG-----KONST----MFLTPENSWTPKACVIVYIEDDG 540
Db 490 LKLSFYLLINAKGIVRTGTHGLLVKQEDMKHFSISIPVKSIDIAPVAPARLLIYAVLPTG 549
QY 541 EIIISDLVKIPVLVFNKIKLYKSKVKAEPSEKVSIRISVTPQDSIVGIVAVDKSVNLMN 600
Db 550 DVIGDSAKYDVENCLANKVDLSFSPSQSLPASHAHLEVTAA-POSVCALRAVDQSVLLMK 608
QY 601 ASNDITWENVHEL-ELYNTGY-----YLGFMFMS-----FA 631
Db 609 PDAELSSASSYNLLPEKDLTGFPGLDQDDDEDCINRHNHYINGITVTVSSTNEKDMYS 668
QY 632 VFOECGLWLTDANLTKDYIDGVYDAAE-----YAEFMEENEGHIVDIHDPSL 680
Db 669 FLEDMLKAFNKGIRKPKPCPOLQOYEMMGPEGLRVGFYESDVMGRGHARLVHVEE--- 725
QY 681 GSSPH---VRKHFPETWIMLDTNMGXRIYQEFFEVTVPDSITSWVATGFVISEDGLGLTT 737
Db 726 ---PHTETVRKYFPETWIMDLVVVNSAGVAEVGVTPDTITETWKAGAFCLSEADAGLIGSS 782
QY 738 TPVELQAFQFFFLNLPIYSVIRGESEFALBITIFNYLKOATEVKVILIEKSDKFDILMTSS 797
Db 783 T-ASLRAFOFFVELTMPYSVIRGEAFTEKATVNLPLPKCIRVSVQLEASPAFLAVPVEK 841
QY 798 E-----INATGHQOQLLVPSDEGATVLPFRPHLGEIPITVIALS-----PTA 841
Db 842 EQAPHICICANGRO-----TVSWAVTPKSLGNVNPVTSAALESQELCGTEVPSV 890
QY 842 -----SDAVTQMILVKABGIEKYSOSIILDLTDNRLQSTLTLSPFPPTVTGSEVRO 896
Db 891 PEHGRKDTVIKPLLVPEPEGLEKETTFNSLLCPSGGEVS---EELSILKLPNVVEESARAS 947
QY 897 ITAIGDVLGPIINGLASLIRMPYCGCEQNMINEAPNIYIILDYLTKKQLTDNLKELASF 956
Db 948 VSVGLILGSAMQNTQULLQNPYCGCEQNMVLPAPNIYVLDYLNQTLTPEIKSKAIGY 1007
QY 957 MRQGYORELYQREDGFSFAG-NYDPS-GSTWLSAFVLCFLEADPYIDIDQNVLHRTY 1014
Db 1008 LNTGYORQLNYKHVDSYSTFGERYGRNQGNWTWLTAFVLKTPAQARAYIFIDEAHITQAL 1067
QY 1015 TWLKGHKQKNGEFDGRVTHSELOGGNKSPWLTAYIVTSLIGYKYPQPNIDVQBSIHF 1074
Db 1068 IWLQRQKONGCFRSGSLNNAIKGVEDEVLSAYITIALLEIFLTVTHPVVRNALFC 1127
QY 1075 LES-----BFSRGISDNYTLALITYALS SVGS-PKAKZALNMLTWRAEQEGMQFW--- 1124
Db 1128 LESAWKTAQSGDHG-SHVYTKALLAYAFALAGNQDKRKEVKLSINEEAVKKONSVHWERP 1186
QY 1125 VSSSEKLSDSWQPR--SLDIEVAAYALLSHFLOFO---TSEGIP-----IMRWLSQRNSL 1175
Db 1187 QKPKAPVGHFEPQAFSAEYEMTSYVLLA-YLTAQAPAPTSEDITSATNIVKWKITQOONAQ 1245
QY 1176 GGFASDTQDTTVALKALSEPAALMNTERTNIQVTVTGPSPSPPLAVQO----- 1222
Db 1246 GGFSSSTQDTTVALHALSKYGAATFT-RTGKAQVTTIOSSGTFSSKFQVDNNRLLLOQVS 1304
QY 1223 ----PMAVNISANGFGFAICQLNVVYNVKASGSSRRRSRISQNOEAFDLDVAVK---ENKD 1275

Search completed: August 10, 2004, 19:39:06
Job time : 65 secs

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GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: August 10, 2004, 19:25:04 ; Search time 23 Seconds
(without alignments)
3205.299 Million cell updates/sec

Title: US-10-020-095-4
Perfect score: 7348
Sequence: 1 MQGPPL2TAHLLCVCTAL.....HSSVIFPCFKLLYFMELWL 1428

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 389414 seqs, 51625971 residues

Total number of hits satisfying chosen parameters: 389414

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : Issued Patents AA:*
1: /cgn2_6/prodata/2/iaa/5A COMB.pep.*
2: /cgn2_6/prodata/2/iaa/5B COMB.pep.*
3: /cgn2_6/prodata/2/iaa/6A COMB.pep.*
4: /cgn2_6/prodata/2/iaa/6B COMB.pep.*
5: /cgn2_6/prodata/2/iaa/PCTUS COMB.pep.*
6: /cgn2_6/prodata/2/iaa/backfiles1.pep.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	1441	19.6	1474	US-09-241-606-2	Sequence 2, Appl
2	973.5	13.2	1651	US-08-447-411-2	Sequence 2, Appl
3	931	12.7	1663	US-08-793-126-1	Sequence 1, Appl
4	931	12.7	1663	US-09-132-271-1	Sequence 1, Appl
5	931	12.7	1663	US-09-142-334-22	Sequence 22, Appl
6	921	12.5	1676	US-08-487-283A-2	Sequence 2, Appl
7	894	12.2	1642	US-08-662-227-2	Sequence 2, Appl
8	894	12.2	1642	US-09-017-947-2	Sequence 2, Appl
9	894	12.2	1642	US-09-925-442-2	Sequence 2, Appl
10	885	12.0	1642	US-08-447-411-45	Sequence 45, Appl
11	880	12.0	1648	US-08-662-227-35	Sequence 35, Appl
12	880	12.0	1648	US-09-017-947-35	Sequence 35, Appl
13	880	12.0	1648	US-09-925-442-35	Sequence 35, Appl
14	768.5	10.5	1333	US-08-447-411-76	Sequence 76, Appl
15	758.5	10.3	1333	US-08-662-227-34	Sequence 34, Appl
16	758.5	10.3	1333	US-09-017-947-34	Sequence 34, Appl
17	758.5	10.3	1333	US-09-925-442-34	Sequence 34, Appl
18	329	4.5	645	US-07-779-172A-3	Sequence 3, Appl
19	271	3.7	1667	US-09-489-039A-11624	Sequence 11624, A
20	234	3.2	113	US-09-311-352B-2	Sequence 2, Appl
21	215.5	2.9	250	US-09-241-606-4	Sequence 4, Appl
22	211.5	2.9	1716	US-09-543-681A-7609	Sequence 7609, Ap
23	185	2.5	183	US-09-311-352B-4	Sequence 4, Appl
24	185	2.5	183	US-09-543-681A-6304	Sequence 6304, Ap
25	180	2.4	1341	US-09-252-991A-26785	Sequence 26785, A
26	177.5	2.4	2777	US-09-543-681A-6124	Sequence 6124, Ap
27	174.5	2.4	2366	US-08-480-604A-10	Sequence 10, Appl

ALIGNMENTS

RESULT 1
US-09-241-606-2
; Sequence 2, Application US/09241606
; Patent No. 6472140
; GENERAL INFORMATION:
; APPLICANT: Tanzil, Rudolph E.
; APPLICANT: Kovacs, Dora
; APPLICANT: Saunders, Aleister J.
; TITLE OF INVENTION: Alpha-2-Macroglobulin Therapies and Drug Screening Methods for
; TITLE OF INVENTION: Alzheimer's Disease
; FILE REFERENCE: 0609.4460003
; CURRENT APPLICATION NUMBER: US/09/241.606
; CURRENT FILING DATE: 1999-02-02
; NUMBER OF SEQ ID NOS: 27
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 2
; LENGTH: 1474
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-241-606-2

Query Match	19.6%	Score 1441	DB 4	Length 1474
Best Local Similarity	29.1%	Pred. No. 7.7e-111		
Matches	451	Conservative	266	Mismatches 551; Indels 284; Gaps 59
Qy	12	LLCVCTAALAVAGPRFLVTPAGIIRPGGNVTIGVLELHCPQSVTVKAEILLKTASLTV	71	
Db	15	LLVLLPTDASVSGRPQYMLVPSLLHT-ETTEKGCVLLSYLNETVTVSASLESYRGNRSL	73	
Qy	72	-SVLEAEG-VPEKGSFKTLTLPSPKNSADP--IYELRVTRGTODEILPNSNTRLSFET	126	
Db	74	FTDLEANDVLHCVAF-----AVPKSSNEEVFLTVQVKGTOE---FKKRTVMVKN	124	
Qy	127	KRISVFIOTDALKYKQEVKFRIVTVFSDPKPYKTSNLIL-INKPKSNLIQOQLSQOSD	185	
Db	125	EDSLVFVQTDKSIYKPGQTVKFRVVSMDENPHNLPLIPLVYIQDPKGNRIAQWQSFOL	184	
Qy	186	LGVTSKTFLSHHILGDWSIQVQVND--QTVYQSFQVSEVLPKFEVTLQTPLYCSMNS	243	
Db	185	GGLKQFSPFLSEEFQGSYKVVVQKSGGRTEH-PFTVEEFVLPKFEVQVTPVKIITILE	243	
Qy	244	KHLNGTITAKTYGKPYKGDVTLTFLPL-----SFMGK	276	
Db	244	EEENVSVCGLYTKPVPVGHVTVSICRKYSDASDHGDSQAFCEKFGQLNSHSGCFVQ	303	
Qy	277	KXNTKFKKINGSANFSDNDDEEMQNVMDSSNGLSEYLDLSPGPEVILT-----TVTESV	331	
Db	304	VK--TKVFQLXR-----KEYEMK-----LHTEAQIQEGTVELTGRQSSEITRTI	347	
Qy	332	TGISRNVTSTNVFFKQHDYIIEFFDYTTVLKPSLNFATVTKVTRADGNQLTLEERNRWI	391	

Db 348 TKLS-PVKVDHFRQG--IPFFG-----QVRLVDGKGVPIP-----NKVI 384
Qy 392 TVQBNYTEWSSNSNGQKQWAVO-KINYT--VPOSGIFKIEFP-----ILED5 438
Db 385 FI-RGNEANYI--SNATTDSHGLVQFSINTNVGTSITVRVNYKDRSPCYGQWVSEEH 441
Qy 439 SEIQLKAYFLGSKSSMAVHSLFKSPSKTYIQLKTRDENIKVGS-----PPELVVSGNK--R 492
Db 442 EEAHTAY-----LVFSPSKSFVHLEPMSHELPCGHTQTVQAHYILNGGTLG 489
Qy 493 LKELS--YMWVSGQLVAVG-----KONST-----MPSLTPENSWTPKACVIVYIEDDG 540
Db 490 LKXLSFYLLIMAKGIVRTGHLGLLKQEDMKGHFISIPVKSADIAVARLLIYAVLPTG 549
Qy 541 EITSDVLKIPVOLVFNKIKLYKSKVKAEPSEKVSIRISVTQDSIVGLVAVDKSVNLWN 600
Db 550 DVIQDSAKYDVENCLANKVDLSFSPQSLSASHAHLVTPAA-POSVCALARAVDOSVLLMK 608
Qy 601 ASNDITMENVVEL-ELYNTGY-----YLGFMFMS-----FA 631
Db 609 PDAELSASSVNLPEKDLGFGPLNDQDEDCINRHNVIYINGITYTPVSVSTNEKDMYS 668
Qy 632 VPQEGHVLTDANLTKDYIDGVYDNAB-----YAEFMEENEGHIVDIDHDFSL 680
Db 669 FLEDMGUKAFTNSKIRPKKPCPOLQVEMHGPGLRGVGFYSDVMGRGHARLVHVEE--- 725
Qy 681 GSSPH---VRKHFPETWILDTMNGYRIYQEFVTPDSITSWATGFWISEDGLGLTT 737
Db 726 ---PHTETVRKYRPEITWDLVVNSAGVAEVGVTPDTITENKAGAFCLSEADAGLGISS 782
Qy 738 TPVELQAFQPPFIFLNLPSVIRGEBEPALEITFNYLKDTEVKKVILEKSDKFDILMTSS 797
Db 783 T-ASLRAFQPPFVELTWPYSVIRGEAFTLKATVNLVLPKICIRVSVQLEASPAPLAVPEK 841
Qy 798 E-----INATGHOQTLLVPSEGDATVFPFIRPHLGEIPITVIALS-----PTA 841
Db 842 EQAPHCICANGRO-----TVSWAVTPKSLGNVNFVSAALESQELCGTEVPSV 890
Qy 842 -----SDAVTQMLVKAEGTEKYSQSLDLDNRLOSTLTKLSFPFNPNTVTSRVRQ 896
Db 891 PEHGRKDTVTKPLVVEPEGLEKETTFNSLCPGSGEVS---EELSXLKLPNVVEESARAS 947
Qy 897 ITATGDLVPSINGLASLIMPYCGGONMINAPNIYILDYTKKKOLTDN:KERALGF 956
Db 948 VSLGDLGSAWQNTQNLQYPCGQGNMVLFPAPNIYLDYNETQQLTPEIKSAIGY 1007
Qy 957 MRQGYORELLYQREDSFSAFG-NYDPS-GSTWLSAFVLCFLEADPYIDIDQNLHRTY 1014
Db 1008 LNTGYQRLNYKHYDGSYSTFGERYGRNQNTWLTAFVLKTAQARAYIFIDEAHITQAL 1067
Qy 1015 TWLKGHOKSGEFDHPRGVHSELOGGNKSPVLTIVTISLLGYRKYQENIDQSSIH 1074
Db 1068 IWLQKQKNGCFRSGSLLNNAIKGQDEVTLSAYITIALLEIPLVTHVTVVRNALFC 1127
Qy 1075 LES-----BPSRIGISDNYLTALITYALSSVGS-PRAKEALNMLTWRAEOEGMGQFV--- 1124
Db 1128 LESAWKTAQBGCHG-SHYTYKALLAYAFALAGNODKEVYKLSNEEAVKKNDSVHWERP 1186
Qy 1125 VSSSKLSQSDQPR--SLDTEVAAYALLSHFLQFQ-----TSEGIP-----IWRWLSROGNSL 1175
Db 1187 QKPAPYGHFEPQAPSAEEMTSYVLLA-YLTAQPAPTSEDTSATNIVKWTQCNQAQ 1245
Qy 1176 GGFASOTDTTVALKALSEFAALMNTERTNIQVTVTGSPSPSLAVQO----- 1222
Db 1246 GGFESTQDTTVALHALSKYGAFT-RTGKAAQVTIQSSGTFSSKQVQDNNELLQQVS 1304
Qy 1223 ----PMAVNTSANGFPAICOLNVVNVKASGSSRRRS:QONQAFDLDVAVK---ENKD 1275
Db 1305 LPPELPGYSMKVTGCGVYLQTSIKYNI-----LPEKEEFPFALGVQTLFQTC 1353
Qy 1276 DLN-HVDLNVCTSFSGPG---RSGVALMEVNLISLGFMPVPEASLSL---SETVKVYDYG 1328

Db 1354 EPKAKTSFQISLSVSYTGSRSSASNAIVDKVMSGFIPLKPTVKVCLERSHNVSRTEVSSN 1413
Qy 1329 KINLYLDSVNETQFCVNIAPAVRNEKVSNTQDASVSIVDYIEPRRQAVRSYNS 1380
Db 1414 HVLVLYDKVSNQTLISLFTFVLQDVPVRLKPAIVKVVDYIETDEFAIAEYNA 1465
RESULT 2
US-08-447-411-2
; Sequence 2, Application US/08447411
; Patent No. 5773243
; GENERAL INFORMATION:
; APPLICANT: FRITZINGER, DAVID C.
; APPLICANT: BREDEHORST, REINHARD
; APPLICANT: VOGEL, CARL-WILHELM
; TITLE OF INVENTION: DNA ENCODING COBRA C3, CVF1, AND CVF2
; NUMBER OF SEQUENCES: 81
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: OBLON, SPIVAK, MCCLELLAND, MAIER & NEUSTADT,
; ADDRESSEE: P.C.
; STREET: 1755 S. Jefferson Davis Highway, Suite 400
; CITY: Arlington
; STATE: Virginia
; COUNTRY: U.S.A.
; ZIP: 22202
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent in Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/447,411
; FILING DATE:
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/043,747
; FILING DATE: 07-APR-1993
; ATTORNEY/AGENT INFORMATION:
; NAME: Oblon, No. 5773243man F.
; REGISTRATION NUMBER: 24,618
; REFERENCE/DOCKET NUMBER: 1126-101-0
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (703) 413-3000
; TELEFAX: (703) 413-2220
; TELEX: 248855 OPAT UR
; INFORMATION FOR SEQ ID NO: 2:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 1651 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
US-08-447-411-2
Query Match 13.2%; Score 973.5; DB 1; Length 1651;
Best Local Similarity 23.5%; Pred. No. 1.2e-71;
Matches 391; Conservative 278; Mismatches 649; Indels 343; Gaps 61;
Qy 1 MCGPPLLTAALHLLCVCTAALAVAPGPRFLVTPAGIIRPGNVITIGVELL-EHCPSQVTVK 59
Db 1 MEGVALVLAALLIGFPGS---SHGALVTLITPAVLRDTEEQILVEAHGDSSTPKSLDIF 57
Qy 60 A-----ELLKTKASNLTVSVLEAGVFEKSGFKTLILPLSLPINSADIEYELRVGTQDEIL 115
Db 58 VHDTPRKQKTLFQSRVDMNQAGSMFVT---PTIKVPAKELNKSQKQVYVVKVGTGQVA 114
Qy 116 TSNRSLSFETKRIKSVFTQTDKALYKPKQEVKFRIVTLFSDFKPKYKSLNILLIKDKPSNL 175
Db 115 LEKVLLSYQSG--FVFIQTDKGIYTPGSPVRYRFSV--DHNHMRMDKTIVE----- 164
Qy 176 IQQWUSQSDLGIVSKTKTQLSHSHP1-----LGDWSIQVQVN---DOTYY 216
Db 165 -----FQTPGIV-----VSKFVNPSSGIRPNYLPVLSFGTWKAVAKYEHSPESYIT 213

Qy	217	QSQVSEYVLPKEVTLQTP---LYCSMNSKHLNGTTAKYTYGKPKVKGVDVTLTFLPLSPF	273
Db	214	AYFDVREYVLPSEVRLQPSDKFLYIDGN-KNFHVSITARYLYGKKEVG-VAFVVFVGVI	271
Qy	274	WGKKNI-----TKTEFKINGSANFSFDEEMKVMVDSNGLSEYLDLSSPGVEILITVTE	329
Db	272	DDAKKSIPDSLTRIPIIDGGEATLKEDTLRSRFQDLNLQLVGHTLYVS-----VTVITE	325
Qy	330	SVTGISRNVTNVFFKOHDYIIFFDVTTVLKPSLNFTATVKVTRADGNOLTEERRNV	399
Db	326	SGSDMVVTEQGGHIVTSPQIVFTKPKFKGMPVELTVYVTVNPDGSPAA-----H	378
Qy	390	VITVTORNVTYEWGSGNQKQEAOKINYTP--QSGTEKIERPILSDSSELQKAY	446
Db	379	VPVSEAIHE-----GTTLSGTAKLILNPLNIQS-----LPIVTRNHGDLPRE	425
Qy	447	FLGSKSMVAHSLFKSPSKTYIOUKTRDENIKVGS--PFELVYSGN---KRLKELSYMV	500
Db	426	RQAIKSMATAYOTQGGSENYLHVAITSTETIKPGDNLNVNFNRGNANSLNQIKFYILI	495
Qy	501	VSRGQLVAVGK-----ONSTMESLTPENSKTPKACVIVVYIEDDGEILSDVLKIPVQ--	552
Db	486	LNKGKIFKVGQRPRDCQNLVTWNLHITPDLIISFRFVAYIQVGNNEIVADSVVWDVKOT	545
Qy	553	----LVFK-----NKIKLYMSVKABEPSKVSLRISVTPDSITGVIVAVDKSVLNMAS	602
Db	546	CMGTFLVVGASSRDDRQ-----KEGAAMKIKLE-GDPGARVGLVADVAKVYVLNDK	596
Qy	603	NDITMENVHELELYNTGYLGMFMSFANFOBCGLWLTDAMLT-----	647
Db	597	YKISQAKIWDTIEKSDFGCTAGSQNNLGVFDAGLALTSTNLNTKQRSAAKCPOPANR	656
Qy	648	-----XDYIDGVVDN-----AEVAERMEENEG-----	670
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Qy	671	--HIV-----DIHDFSJGSSPHV-RKHPPETWIL-----DTNMG	702
Db	717	CCHYKIRDENORESELFLARGDFDELFGDDNIIERSDFPESWMLTBELTCEPNMQ	776
Qy	703	YRIQBEFVTP--DSITSWATGVFISEDGLGLTIT-----PVLEQAFQPPFIF	751
Db	777	IS-----SKTVPYLRDSIITW-----ELAVGLSPTKGCVABEYBITVKNKOFFID	823
Qy	752	LNLPYSVIRGEEFALETIFNYLKDATEVKVITIEKSDKFDILMTSSINATGHQTLTLP	811
Db	824	LRLPYSVVVKEQVEIRAILLYNADEDIYRVVELIYNPAF---CSASTEGRYRQOPPIK	879
Qy	812	SEDGATVLPFIRPHLG--EIPITVLTALSTADAVTOMILVKAEGTEKYSQSILDLT	869
Db	880	ALGSRAVPFVIVPLEQGLHDEVIASVRGELASDGVEKKLVVPEGBERKNIVTIIELDPS	939
Qy	870	DNRLQST--LKTLSFSPFPNTVTSERVQITAGD---VLGFSING--LASLIRMPYGC	921
Db	940	VKGVGGTQELTVIANKLDDKVPDTEVETRISVLGDVPAQIIENSIDGSLNHLIITPSGC	999
Qy	922	GEQNMINFANI---YILDYTKKKQLTDNLKEALSFMRQCGTQRELLYQREDSGSAFG	978
Db	1000	GEQNMITPESVATYATYLDATQWENELGVDRTEAIRQIMTGYAQOMVYKKAHSAAF	1059
Qy	979	NYDPSGWTLSAFVLRCLFLEADPYI-DIDQNLVLRHTVTL-KGHOKSGNEFFWDPGRVHS	1036
Db	1060	N--PASSSWLTAYVVKVLAMASNVMKDI SHEIICGGVKWILLNKEQPDGVFKENAPVHIG	1117
Qy	1037	ELOGGNKS---PVTLTAYIVTSLGKYRKYQNDIVQBSIHFLSEFSERG-----I	1083
Db	1118	EMLGGTKGABPEASLTAFITALESRSV-----CKEQINLDSINKATDYLLKKYEKL	1172
Qy	1084	SDNYTALITVYLSVSGPRAKEALNMLTWRAELEGCMQFWVSSEKLSDSMQPSRLDIE	1143
Db	1173	QRPVTTALTAYALA-----AADRLNDRVLMAASTGNRW-----SEYNARTHIE	1218
Qy	1144	VAAYALLSHFLQFOTSEGIPIMRWLSRQNSLGGFASTQDITVALKALSFAALMNTER-	1202

Db	1219	GTSYALLALMKKFAEVBGVFWRLIDQKYGGTYGQTQATVMVFOALAEYEQMPTHQD	1278
Qy	1203	TNTQVTVGPSSPSP-----LAVQPMAV-----NISANGFGFATCQLNVVYNVK	1247
Db	1279	LNLDSIKLPREVPERYSINDRNAQARIVETKLNEDFTVVSAGDGKATMTILTVMNAQ	1338
Qy	1248	ASGSSRRRRSIQOEAFDLDVAV-----KENKDDLNVLDLVNCTVSFSGPGRSGMALME	1300
Db	1339	L-----REDANVCNK--FHLDSVENVELNLKQAGKGAALRLICTRYLGEVSTMTIID	1392
Qy	1301	VNLLSGFMVPSBAI-----SLSTVVKVEVDH-----GKLNLYLDSVNETQ--ECVNIIPAV	1349
Db	1393	ISMLTGFPDAEDLKLNSGVDRYISKFEIDNNNAQKGTVIYLDKVSHSEDECLFKIHH	1452
Qy	1350	RNFKVSNTODASVSIVDYIEPRQAVRSYNSVKLSSCDLCSVDQGPCPEDCAGSGSHH	1409
Db	1453	KHFEVGFIOGSKVVKVSYYNLDQCTKFYHPDKETGLLNKI CHGNICRCAEETCSLLNQ	1512
Qy	1410	-----SSVIFICFCKLL-----YFMEL	1426
Db	1513	KKIDLQRIOKAQNVDYVYKTKKLARIEBKQGNDIYFMDV	1553

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Query Match 12.7%; Score 931; DB 2; Length 1663;
Best Local Similarity 23.0%; Pred. No. 4.5e-68;
Matches 376; Conservative 286; Mismatches 615; Indels 356; Gaps 62;

QY 3 GPPILTAHLLCVCCTAALAVAPGPRFLVTPGIIR-----PGNVTIGVELL 49
||| ||| ||| ||| ||| ||| ||| ||| ||| ||| : : : : :
db 6 GPSLL----LLLLTHPLALG-SPMYSIITNLRLSEETWVLAEHPAQGDVPVTVTH 60

Query Match

[illegible]

943	AV-RILDPELREGVQKE--DIPPAD:SDQVPDTESETRILLQQTTPVAQMTEDAVDAE	998
911	-LASIRMPYGCGEQNMNFANIVILDTKKKQJTDNLKKE---ALSFMEQGYORELL	966
999	RLKHLIVTSPGCGEQNMIGMTPTVIAVHYLDLDETEQWEKFGLEKQGALEILIKGYTQQA	1058
967	YQREDCGSFAFCNYDPGSGTWLSAFVLRCFLADPVIDIDQNVLHRTYFWL-KGHQKSMG	1025
1059	FQPPSSAFAAFVKRAP--STWTAIVVVKVPSLAVNLIAIDSVLCAVFWLILEKQKPDG	1116
1026	EFWDPCRVHSELQCG---NKSPVTLTAIYIVTSLGVRYKYPQNDIV-QESTH-----	1073
1117	VQEDAPVHQEWIGLGRNNEKDMALTAFLISL-----QEAQDICEQVNSLPGSIT	1170
1074	----FLESEFSGISDNVTYLTALITYLSSVGSFKAKEALNMLTWRAEQEGGQFWVSSSES	1129
1171	KAGDFLEANY-WMLORSYTVIAGVALAQMGRKGLPLLNKFLT-----TA	1214
1130	KLSDSQWQ---PRSLDIEVAAYALLSHFLQFQTSSEGI-PIRMWLSRQNSLGGFASFTQDTT	1185
1215	KDKRNEWDGKQLYNVEATSALLA-LLQKDFDVPVPPVVRMLNEQRYGGVYSTQATF	1273
1186	VALKALSEFAA-LMNTFRNIOVTVTGPSSPSPLA-----VVQPMAVNIS	1229
1274	MVFQALAQKQDAPHQEQLNLDVSLQLPSRSSKITHRIEWSASLLRSBETKENEFTVT	1333
1230	ANGFPAICQLNAVNVNKGASGSSRRRSIQNEAFDLDVAV-----KENKDDLNVLDL	1282
1334	ASGKGQGLSVTWMHAKAKDQTCNK-----FDLKVIRKAPATEKRPQDAKNTMIL	1386
1283	NVCTSPSGRSGMALMEVNLISGFMVPSB-----AISLSETVKVKEY-----DHCKLNL	1332
1387	EICTRYRGQDQMTSLDISMTGEPADTDLKQLANGVDVRYISKYELDKAFSDRNTLII	1446
1333	YLDYSVNETQ-FCWNPVAVNFVKSNTODASVSIVDVYEPRRQAVRSYNSSEV---KLSSCD	1388
1447	YLDKVSHSDDCLAFKVHQYFNVELIQGAVKVYAYINLEESCTRFYHPEKEDGKLNK--	1504
1389	LCSDVQGCRCPCED	1401
1505	LCRD-ELCRCAEE	1516
RESULT 6		
US-08-487-283A-2		
; Sequence 2, Application US/08487283A		
; Patent No. 6355245		
; GENERAL INFORMATION:		
; APPLICANT: Evans, Mark J.		
; APPLICANT: Matis, Louis A.		
; APPLICANT: Mueller, Eileen Elliott		
; APPLICANT: Nye, Steven H.		
; APPLICANT: Rollins, Scott		
; APPLICANT: Rother, Russell P.		
; APPLICANT: Springhorn, Jeremy P.		
; APPLICANT: Squinto, Stephen P.		
; APPLICANT: Thomas, James A.		
; APPLICANT: Wilkins, James A.		
; TITLE OF INVENTION: METHODS AND COMPOSITIONS FOR THE TREATMENT		
; OF INFLAMMATORY DISEASES		
; NUMBER OF SEQUENCES: 26		
; CORRESPONDENCE ADDRESS:		
; ADDRESSEE: Seth A. Fidel		
; STREET: 25 Science Park (Alexion)		
; CITY: New Haven		
; STATE: Connecticut		
; COUNTRY: USA		
; ZIP: 06511		
; COMPUTER READABLE FORM:		
; MEDIUM TYPE: 3.5 inch, 1.4Mb storage		
; COMPUTER: Macintosh Cetrus 610		
; OPERATING SYSTEM: System 7		
; SOFTWARE: WordPerfect 3.0		

QY 1233 FGFAICQLNVVNVKASGSSRRRRSTQOAFDLVAVKENKDDLNHVD-----INVCT 1286
Db 1318 DGKATWILTLYNAQL-----QEKANCNK--FHLNVSE--NIHLNAMGAKGALMLKICT 1369
QY 1287 SFGSGRSGMALMEVNLGSEWVPSAIS-----LSETVKVEYDHGKLN-----LYLDS 1336
Db 1370 RYLGEVDSTWITIDISNLGFLDPAEDLRLSGVDRIYSRIEVDNMAQKAVAVIILNK 1429
QY 1337 VNETQ--FCVNIAPVRNFKVNSNTQDASVSDVYEPYPRQAVRSYNSEVKLSLSCDCLSDVQG 1395
Db 1430 VSHSEDECLHFKILKHFEVGFQPGSVKVVSYNLDEKCTKFVHPDKGTGLLNKICIGNV 1489
QY 1396 CRCECEGASGSH-----HSGVIFPCFKLIYPWE 1425
Db 1490 CRCAGETCSLNHQRIDVPLQIEKACETNVDVYTKLIRIE 1533

RESULT 8
US-09-017-947-2
; Sequence 2, Application US/09017947
; Patent No. 6303754
; GENERAL INFORMATION:
; APPLICANT: VOGEL, CARL-WILHELM
; APPLICANT: BREDEHORST, REINHORST
; APPLICANT: KOCK, MICHAEL
; APPLICANT: FRITZINGER, DAVID
; TITLE OF INVENTION: RECOMBINANT PROCVF
; NUMBER OF SEQUENCES: 39
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: OBLON, SPIVAK, MCCLELLAND, MAIER & NEUSTADT,
; STREET: 1755 S. JEFFERSON DAVIS HIGHWAY
; CITY: ARLINGTON
; STATE: VA
; COUNTRY: USA
; ZIP: 22202
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/017,947
; FILING DATE:
; CLASSIFICATION:
; PRIOR APPLICATION DATA: US 08/662,227
; FILING DATE: 14-JUN-1996
; ATTORNEY/AGENT INFORMATION:
; NAME: OBLON, NORMAN F.
; REGISTRATION NUMBER: 24,618
; REFERENCE/DOCKET NUMBER: 1126-0107-0X
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 703-413-3000
; TELEFAX: 703-413-2220
; INFORMATION FOR SEQ ID NO: 2:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 1642 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: protein
US-09-017-947-2

Query Match 12.2%; Score 894; DB 4; Length 1642;
Best Local Similarity 22.5%; Pred. No. 5.5e-65;
Matches 361; Conservative 295; Mismatches 672; Indels 276; Gaps 56;
QY 18 AALAV-----APGPRFLVTPAGHIRPGGNVTIGVELL-EHCPSQVTVKA-----ELIKTAS 67
Db 10 AALLIGPPGSHGALYTLITPAVLRTDTEQILVEAHGSDTPQLDIFVHDPKQKTLF 69

QY 68 NLTVSVLEAEGVFKGSEKTLITLPSLPLNSADEIYELRVTRTQDEILFNSSTLSSETK 127
Db 70 QTRVDMNAPAGMLVT---PTIEIFAKEVSTDSRQNVVQVTVQFQVLEKLVLSYQSS 126
QY 128 RISFIQTDKALYKPKQEVKFRIVTLFSDFKPYKTSNLILKDKPSNLIOQLWLSQQSDLG 187
Db 127 --FLFIQTDKGIYTPGSPVLVRFVSMDBHNTSKNKTIVVEFQTPEGILVS---SNSVDLN 181
QY 188 VISTFQLSSHPHIGDWSI--OVQNDCTYYQSQVSEYVLPKFEVTLQTP---LYCSMN 242
Db 182 FF-WPYNLPDLVSVLGTWRIVAKYSEHPENYATAYEDVAKYVLPSEFVRLQPSKEKFYIDGN 240
QY 243 SKHLNGTITAXVYTKPKVKGVDVTLTFLPSFWGKKNI---TKTEKINGSANFSFNDEE 298
Db 241 -ENFVSTIARYLYGEEVEG-VAFLVGVKIDDAKSIIPDSLTPIPIIDGDKATLXRD 298
QY 299 MKNVMDSSNGLSEYLDLSSPGFVEILTFTVTSVTGISRNVTNVTFFKQHDVIIFFPYTT 358
Db 299 PRSRFPNLNLVGHITLYAS-----VTVMTESGDMVVTQSGIHIIVASPYQIHFTKTPK 352
QY 359 VLKSLAFTATVKYTRADGNQLTLEERRNNVIVITQNTYEWGSGNSGNQKVEAQKI 418
Db 353 YFKPGMPYELTVYVTPNPDGSPA-----AHVPVSEAF-----HSMGTTLSDGTAKL 398
QY 419 NYTVPSQSGTFKIEFPFILEDSSELQKAYFLGSKSMVHSLFKSPSKTYIQLKTRDENIK 478
Db 399 ILNIPLNAQ---SLPITVTRTNHGDLPREKQATKSMALAYQOTGSGNYLHVAITSTEIK 455
QY 479 VGS--PFELVSGN---KRLKELSYVMVSRGQLVAVGK-----QNSTMPSLTPENSWT 526
Db 456 PCDNLPVNFNVKGNANSLKQIKFYTLILNKGIKFKVGRQPRRDQGNLVTNHLHITPDL 515
QY 527 PKACVIVYVIEDDGEIISDLVKIPVQ-----LVFK--NKILYMSKVKAEPSEKVSURI 578
Db 516 PSFRFVAYQVGNNEIVADSVVDVKOTCMGTLVVKGNLIOM-----PGAAMKIL 567
QY 579 SVTPQDSIVGIVADKSVNLNANSDITMENNVHELELYNTGYKLGMPMSFAVQBQGL 638
Db 568 E-GDPRARGLVAVDKAVYVLDNKYKISOAKIMDTIEKSDFGTAGSQNNLGVFEDAGL 626
QY 639 WVLTDANL-TKD-----649
Db 627 ALTTSTNLNTKQSAKCPQANRRRRSSVLLDSNASKAAEFQDQDLRKCCEDVMHNP 686
QY 650 -----YIDGYD-NAEYAEFRM--EENE-GHIVIDHDF 678
Db 687 MGYTCEKRAKYIQEGDACKAFLCCRYIKGVRDENQRESEFLFLARDNEDGFIADSDII 746
QY 679 SLGSSPHVRKHPPETWIWL-----DTNMGRIYQEFVTPDTSITSWATGFISEDLG 732
Db 747 S-----RSDFPKSWLWLTKDLEEPSQGISSKTMSFYLRDSITTTWVLAVSFTPTKG 799
QY 733 LGLTTTPVELOAFOPFFFLNLPYSVIRGEBFALEITIFNLYKDATEVKVIEKSDKFDI 792
Db 800 I-CVAEPEIRVMKVFFIDLPMPYSVVKNQEVETRAILHNVNEDIYVRVELLYNPAF-- 856
QY 793 LMTSEINATGHQQTLLVPSBDGATVPIPIRPHLG--EIPITVTALSP7ASDVTQML 850
Db 857 --CSASTKGQRYRQOPPIKALSRAVPFVIVLEPQGLHDEIKASQVSEALSDGVKXKL 914
QY 851 VKAEGIEKSYQSILLDLTDNLQST-----LKTLSFSPPTNTVTGSEVQITAIQDVL 904
Db 915 VVPEGVQKSIYTVIYKLDPRKGVGTQLEVIKAKLDRVDPDTIETKIIIQGDFVAQII 974
QY 905 GPSING--LASLIRMPYCGCGQNNMINFAPNI---YILDYLTKKKQLTDNLKELSNFRQ 959
Db 975 ENSIDGSKNLHLIITPSCGCGQNNMIRMAAPVATVYLDTTTEQWETLGINRRTEAVNQIVT 1034
QY 960 GYQRELLYQREDDGSPSAGNYDPGSGTWLSAFVLRCP-LEADPYIDIDQNVHRTYTWL- 1017
Db 1035 GYAQMVKYKADHSHYAAFTN--RASSSWLTAYVVKVFAMAAKMWAGISHEIICGVRWLI 1092
QY 1018 KGHQKSNGEFWDPGRVIHSELQG---GNKSPVTLTAYIVTISLLGYR----KYQPNID--V 1068

1093 LNRQPPGAFKFNAPVLSGTMQGGIOGAEBEVLTAFILVALLESKTCNDYVNSLDSSI 1152
1069 QESITHLESFSGRISDNITLALITYALSSVSPKAKEALNMLTWRAEQGGMQFWVSSR 1128
1153 KKAIVLLKKVEK-LQRPYTTALTAYALA-----AADQLNDRVLMMASTGRDH----- 1201
1129 SKLSDSNQPSRLDEVAAYALLSHFLQFQSEGPINRWLSRNSIGGFASTQDTTVAL 1188
1202 ---EYNAHTNTEGTSYALLALLKMKFQDGTGPIVRMLTDQNFYGETYQQTQATVMAF 1257
1189 KALSEFAALMNTER-TNIQVTVTPSPSPPL-----AVQCP---MAVNT-SANG 1232
1258 QALAEYEQMTHKDLMDITIELDPREVPIRINYENALLARTVETKLNQDITVTASG 1317
1233 FGPAICQNVVYVYKASGSRRRRSIQBAPDLDAVAKENKODLNHD-----LNVCT 1286
1318 DGKATMTILTFYNAQL---QEKANVCNK--FHLNVSV--NIHLNAMGAKGALMKICT 1369
1287 SFGSPGRSGHALMEVNLSCGMPSPSEALS-----LSETVKKVEYDHGKLN-----LYLDS 1336
1370 RYLGEVSTMTIIDISMLTGLPDAEDLTRLSKGVDRYISRYEVDNNMAQKVAIIYLNK 1429
1337 VNETQ-FCVNIPIAVRNFKNQNTQDASVSIVDYEPFRQAVRSYNSEKLSCLSDCSDVQ 1395
1430 VSHSEDECLHFKILKHEVGFQPGSVKVVSYNLDSEKCTKFYHPDKGTGLLNKICIGNV 1489
1396 CRPCEDGASGSH-----HSSVIFFCFLLYFME 1425
1490 CRGAGETCSLHNOERIDVPLQIEKACETNVDVYIKTLRIEE 1533

RESULT 9
US-09-925-442-2
Sequence 2, Application US/09925442
Patent No. 6607897
GENERAL INFORMATION:
APPLICANT: VOGEL, CARL-WILHELM
BREDEHORST, REINHORST
KOCK, MICHAEL
FRITZINGER, DAVID
TITLE OF INVENTION: RECOMBINANT PROCVF
NUMBER OF SEQUENCES: 39
CORRESPONDENCE ADDRESS:
ADDRESSEE: OBLON, SPIVAK, MCCLELLAND, MAIER & NEUSTADT,
P.C.
STREET: 1755 S. JEFFERSON DAVIS HIGHWAY
CITY: ARLINGTON
STATE: VA
COUNTRY: USA
ZIP: 22202
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patent In Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/925,442
FILING DATE: 10-Aug-2001
CLASSIFICATION: <Unknown>
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 09/017,947
FILING DATE: <Unknown>
ATTORNEY/AGENT INFORMATION:
NAME: OBLON, NORMAN F.
REGISTRATION NUMBER: 24,618
REFERENCE/DOCKET NUMBER: 1126-0107-0X
TELECOMMUNICATION INFORMATION:
TELEPHONE: 703-413-3000
TELEFAX: 703-413-2220
INFORMATION FOR SEQ ID NO: 2:
SEQUENCE CHARACTERISTICS:
LENGTH: 1642 amino acids

TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: protein
SEQUENCE DESCRIPTION: SEQ ID NO: 2:
US-09-925-442-2

Query Match 12.2%; Score 894; DB 4; Length 1642;
Best Local Similarity 22.5%; Pred. No. 5.5e-65;
Matches 361; Conservative 295; Mismatches 672; Indels 276; Gaps 56;

QY 18 AALAV-----APGRFLVATGIIRPGGNVIGVELL-EHCPQOVTVKA-----ELLKTAS 67
DB 10 AALLGFGSGHAGLYLITPAVLRTDEEQILVEAGDSTPKQLDIFVHDFPRKQKTLF 69
QY 68 NLTVSVLEAEGVFEKSGFKTLTLPSLPNSADEIYELRVGTQDEILFNSNLSPEK 127
DB 70 QTRVDMNPAGGLVLT---PTIEIPAKEVSTDSRQNYVVQVTPQVRLEKVVLLSYQSS 126
QY 128 RISVFIQTDKALYKPKQEVKERIVTLFSDPKPKYKTSNLILIKDPKSLIQQLSQSDLG 187
DB 127 --FLFIQTDKGIYTPGSPVLIRVFSMDHNTSAMKTVLVEFQTEGILVS---SNSVDLN 181
QY 188 VISKTFQLSSHPILGDSI--QVQVNDQTYQSFQVSEYVLPKFEVTLQTP---LYCSMN 242
DB 182 PF-WPYNLPDLVSLGTWRIVAKYEHSPENYTAIFYDKYVLPSEFVRLQSEKFFYIDGN 240
QY 243 SKHLNGTITAKYTVGKPKGVDTLTLPLSPFGKKKI---TKTFKINGSANFSNDEE 298
DB 241 -ENFHSITARYLYGEEVEG-VAFVLPFGVKTDKAKSIPDSLTIRIPIDGDKATLKRT 298
QY 299 MKVMDSSNGLSSEYDLSSPGPVEILTITVTSVTGIGRNVTSTNVFPKHQDYIIEFFDYTT 358
DB 299 PRSRFPNLNELVGHLYAS-----VTMTESGDMVVVTSQSGIHI VASPIQIHFTKPK 352
QY 359 VLKPSLNFTATVKVTRADGNQTLLERRNNVITVTOYNTYEWGSGNSGNQKMEAVQKI 418
DB 353 YFKGMPYELTVVYVTPDSPA-----AHFVWVSEAF-----HSMGTLLSDGTAKL 398
QY 419 NYTVPSQGTFFKIEPFILEDSELOLKAYFLGSKSMAVHSLFKSPSKTYIQLKTRDENIK 478
DB 399 ILNIPLNAQ---SLPITVTRNHGDLPRERQATKNTAIAYQTQGGSGNYLHVATSTEIK 455
QY 479 VGS--PFELVYSGN---KRLKELSYMVSRGQVAVGK-----QNSTMFLSPENSWT 526
DB 456 PGDNLVFNPNVYKGNANSLKQIKYFTYLILNKGKIFKVGROPRRDGQNLVTMLNHLITPDLI 515
QY 527 PKACVIVYVYIEDGEIISDLKIPVQ-----LVFK--NKIKLYSKVKAEPSEKVSURI 578
DB 516 PSFRFVAYYQVGNNEIVADSVMVDVKDTCMTGLVVGKGNLIQM-----PGAMMKIKL 567
QY 579 SVTQPDSTVIGVAVDKSVNLNANSDITMENNVVHELELYNTGYILGMFMNSFAVQFCGL 638
DB 568 E-GDPGARVGLVAVDKAVYVLDKYSQAKIWDTEI EKSDFGCTAGSGQNNIGVFEDAGL 626
QY 639 WVLTDANL-TKD-----
DB 627 ALTTSTNLNTRQSAKCPQANRRRSVLLLDNSAKAAEFQDQDLRKCCEVWHENP 686
QY 650 -----YIDGVYD-NAEYAEFRM--BENE-GHIVDTHDF 678
DB 687 MGYTCEKEAKYIQSDACKAAFLCECRYIKGVRENQRESELEFLARDNEDGFIADSDII 746
QY 679 SLGSSPHVRKHFPTIWL-----DTNMGYRIYQBEFVTVPSITSVATGVFVISEDLG 732
DB 747 S-----RSDFPKSLMLTKDLTEEPNSQGISKTSFYLRDSITTVVVLAVSFTPTKG 799
QY 733 LGLTTTPVELQAFQPFIFLNLPSYVIRGEFALEITIFNVLKDATBEVKYIEKSDFDI 792
DB 800 I-CVABEYIIRKMFVFDLQMPYSVKNQVEIRAILHNYVNEIDIVRVLYNPAF-- 856
QY 793 LMTSSEINATGHQOITLLVPSEDAVTLFPIRPHLG--EIPITVTLSPASDAVTQMIL 850

Db 857 --CSASTKGORYQOPFIKALSRVFPVIVPLEQGLHVDVEIKASVQEAUMSGVKKUK 914
Qy 851 VKAEGIEKXSQSILLDTNRLQST-----LKTLSFSPPTNTVTSERVQITAGDVL 904
Db 915 VVPEGVQKSVITVKLDPRAKGVGTQLEVIKARKLDRVPDTEIETKIIIQDPAQII 974
Qy 905 GPSING--LASLTPMPGCCGEONINPAPNI---YILDYTKKKQLTDNLKEALSPMQ 959
Db 975 ENSIDGSKLHLIITPSGCCGEONIRVAAPVIATYLDTTQEWETLGINRRTEAVNQIYT 1034
Qy 960 GYORELLYQREDSFSAFGNVDPSGTSWLSAFVLRCP--LEADPYDIDQNVLRHTTWL- 1017
Db 1035 GYACQWYKKADHSYAFTN--RASSWLTAYVVKVPFAAKWAGISHEIICGVRLI 1092
Qy 1018 KHQKSNGEFDPGRVHSELQ--GNKSPVLTAYIVTSLGYR-----KYOPNID--V 1068
Db 1093 LNRQOPDGAFAENAPVLSGTWQGGIOGABEEVLTAFILVALLESKTCINDYVNSLDSII 1152
Qy 1069 QESTHPLESEFSRISGIDNYTALITVALSVSGPKAKEALNMLTWRABQEGGQFVVSSE 1128
Db 1153 KKATNYLLKKYK-LQRPYTTALTAYALA-----AADQLNDRVLMASSTGRDHV- 1201
Qy 1129 SKLSDSQPRSLDIEVAAYALLSHFLQFOTSEGIPIMRWLSQRNSLGGFASQTDTTVAL 1188
Db 1202 ---EYNATHNIEGTSYALLALLKKMKFDQTPGVIRWLTQNFYGETYQTOATWMAF 1257
Qy 1189 KALSEPALMNTER-TNIQVTVTPSPSPPL-----AVQVP---MAVNISANG 1232
Db 1258 QALAEYBIQEPHCKDLNDITIELPREVPIRYINRYENALLARTVETKLNQDITVTASG 1317
Qy 1233 FGFAICOLNVYVNVKASGSSRRRSIQNEAFDLIDVAVKENKDDLHVD-----LNVCT 1286
Db 1318 DGRATWILFYNAQL---QERANVCN--FHLNVSE--NIHLNMGAKGALMKICT 1369
Qy 1287 SPGPGRSAGMALMEVNLISGFWPSEALS-----LSETVKKVBYDHGKLN-----LYLDS 1336
Db 1370 RYLGEVDSTWITIDISMLTGLFPAEDLTRLSKGVDRYISRYEVDNNAQKAVIYLNK 1429
Qy 1337 VNETO-FCVNIAPVRNEKVSNTODASVSIYDVYEPREQAQVRSYNSSEKSLSCDLCSDVQG 1395
Db 1430 VSHSEDECLFKHLKHFEVGFIOGSKVYVSYNLDKCTKTFVHPDKGTGLNKCIGNV 1489
Qy 1396 CRPCEDGASGSH-----HSSVIFFCFKLLYFME 1425
Db 1490 CRCAGETCSLNHQERIDVPLQIEKACETNVVYVYKTLRIEB 1533

RESULT 10

US-08-447-411-45
Sequence 45, Application US/08447411
Patent No. 5773243
GENERAL INFORMATION:
APPLICANT: FRITZINGER, DAVID C.
APPLICANT: BREDEHORST, REINHARD
APPLICANT: VOGEL, CARL-WILHELM
TITLE OF INVENTION: DNA ENCODING COBRA C3, CVF1, AND CVF2
NUMBER OF SEQUENCES: 81
CORRESPONDENCE ADDRESS:
ADDRESSEE: OBLON, SPIVAK, MCCLELLAND, MAIER & NEUSTADT,
ADDRESSEE: P.C.
STREET: 1755 S. Jefferson Davis Highway, Suite 400
CITY: Arlington
STATE: Virginia
COUNTRY: U.S.A.
ZIP: 22202
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/447,411
FILING DATE:

/ CLASSIFICATION: 435
/ PRIOR APPLICATION DATA:
/ APPLICATION NUMBER: US 08/043,747
/ FILING DATE: 07-APR-1993
/ ATTORNEY/AGENT INFORMATION:
/ NAME: Obion, No. 5773243man F.
/ REGISTRATION NUMBER: 24,618
/ REFERENCE/DOCKET NUMBER: 1126-101-0
/ TELECOMMUNICATION INFORMATION:
/ TELEPHONE: (703) 413-3000
/ TELEFAX: (703) 413-2220
/ TELEX: 248855 OPAT UR
/ INFORMATION FOR SEQ ID NO: 45:
/ SEQUENCE CHARACTERISTICS:
/ LENGTH: 1642 amino acids
/ TYPE: amino acid
/ TOPOLOGY: linear
/ MOLECULE TYPE: protein
/ US-08-447-411-45

Query Match 12.0%; Score 885; DB 1; Length 1642;
Best Local Similarity 22.4%; Pred. No. 3.1e-64;
Matches 359; Conservative 296; Mismatches 673; Indels 276; Gaps 56;

Qy 18 AALAV-----APGPRFLVTAQGIIRPGNVITGVELL-EHCPQSQVTVKA---ELLKTAS 67
Db 10 AALLGFGSSHGALYTLITPAVLRTDTEEQLLVEAHGDSSTPKQLDIFVHDFPRKQKTLF 69
Qy 68 NUTSVLBAEGVFEGSKPTLTPLSLNSADEIYELVATGTODEILFNSSTRLSFETK 127
Db 70 QTRVDMNPAAGMLVT---PTIEIPAKEVSTDSRQNYVYVQVTPQVRLKVVLLSYOSS 126
Qy 128 RLSVFIQTDKALYKPKQEVKPRIVTLFSDFKPYKTLNLIKDPKSNLIQWLSSQSDLG 187
Db 127 --FLTIQIDKGIYTPGSPVLKRVFSMDHNTSKNKIVIVEFQTPGILVS---SNSVDLN 181
Qy 188 VISKTFLQSSHPILGDWSI--QVQVNDQTYQSPOVSEYVLPKFEVTLQTP---LYCSMN 242
Db 182 PF-WPYNLPDLVSICTWRIVAKYEHSPENYATFVDRKVVLPSPFEVRLQPKSEKFFYIDGN 240
Qy 243 SKHLNGTTTAKTYTKPKVKGVDVTLTFLPLSPWKKNI-----TKTFKINGSANFNDDEE 298
Db 241 -ENFHVSIATARYLGEVEG-VAFVLFGVKIDDAKKSIPDSLTRIPIDGGKATLKEDT 298
Qy 299 MKNVMDSSNGLSEYLDLSSPGVEVLTVTBSVTGISRNVTNVFPFKQHDVILIEFFDYTT 358
Db 299 FRSRFPNLNVLGHLYAS-----VTMTSGSDMVVTEQSGIHIIVASPPQIHETKTPK 352
Qy 359 VLKPSLNFATVKTTRADGNQILTEERRNNVITVQRNYTEYWSGSGNKGMAVOKI 418
Db 353 YFKPGMPYELTVYVTPDGSFA-----AHVPVYSEAF-----HSMGTTLSDGTAKL 398
Qy 419 NYTVPSQSGTFKIEFFILEDSSSELQKAYFLGSKSMVHSLFKSPSKTYIOLKTDENIK 478
Db 399 ILNIPLNQ---SLPITVTRNHGDLPRERQATKSWTAAYQTQGGSGNYLHVATSTIK 455
Qy 479 VGS--PFELVWSGN---KRLKELSYMVVSRGQLVAVGK-----QNSTMTSLTPENSMT 526
Db 456 PGDNLVPVKFCGCGQCNLSLKQIKYFYILNKGKIFKVGQPRRDQGNLVNMLHTPDLI 515
Qy 527 PKACVIVVYIEDDGEIISDVLKIPVQ-----LVFK--NKIKLYWSKYKAPSEKVSURI 578
Db 516 PSFRFVAYYQVGNNEIVADSVWVDVKTCMGTCLVYKGDNLIQM-----PGAAMKIL 567
Qy 579 SVTQPDSTVIGIVADKSVNLMNASNDITWENVVHELELYNTGYILGFMFNSPAVFEQGL 638
Db 568 E-GDPCARVGLVAVDKAVYVLDNKYKISOAKIWDIEKSDFGCTAGSGQNNLGVFEDAGL 626
Qy 639 WVLTDANL-TKD-----
Db 627 ALTTSTNLTKQRSAAKCPQANRRRRSSVLLSDNSAKAAEFQDQDLKCCEDVYMHENP 686
Qy 650 -----YIDGYVD-NAEYABREFM--EENE-GHIVDIHDF 678

Db 514 LIPSPR--FVAYQVGNNEIVADSVVVDKTCWGLTVKGDNLQMPGAAMKIKLEGDF 571
QY 575 SLRISVTPQPSIYIGIVAVDKSVNLMASNDITWENVVHELELYNTGYILGMFMNSFAVFO 634
Db 572 GAR-----VGLVAVDKAVYVLDNDKYKISAKIWDITKSDFCGTAGSGONNLGVFE 622
QY 635 ECGLWLVTDANL-TKD----- 649
Db 623 DAGLALTSTNLNTKQSAKCPQANRRSSVLLDLSNASKAABFQODLRKCCEDVM 682
QY 650 -----YIDGVVD-NAEVAERFM--EENE-CHIVD 674
Db 683 HENPMGYTCRKAKYIQEGDACKAFLCCRYIKGVDRDENQRESEFLARDNEDGFAD 742
QY 675 IHDFSLGSSPHVKHPETWIML-----DTNMGYRIYQEFFVTVPDSITSWATGVFIS 728
Db 743 SDIIS-----RSDFPKWLMLTKDLTEPNQSGISSKMTSPYLKDSITWVLAVSFT 795
QY 729 EDGLGLTTPVBLQAFQPFIFNLPIYSVIRGEBFALBITFNYLKDATEVKVILKSD 788
Db 796 PTKGI-CVAEPYBIRYMKVFFIDLOMFYSYVKNQEQVEIRAILHNYVYNDIYVRVELLYNP 854
QY 789 KFDILMTSSINATGHOOTLLVPSDGTATVPFIRPTHLG--EIPITVATLSPTASDAYT 846
Db 855 AP-----CSASTKQCRVROQPIKALSRAPVFIIVLEQGLHDEVEIKASQBEALMSDGV 910
QY 847 QMILVKAEGIEKSYOSIILDLTDNRLOST-----LKTLSFSPPTNTVTGSEVQITAI 900
Db 911 KKLKVPPEGVQKSIIVTKVLDPRKGVGGTQLEVIKARKLDDRVPTETETKIIQGDVP 970
QY 901 GDVLGSPING--LASITRMPYGGEGQNMIFANI---YILDYLTKKKQOLDNLKELAS 955
Db 971 AQIENSIDGSKNLHLIITPSGCGEQNMIRMAAPVIATYLDTEQMETLGINRRTEAVN 1030
QY 956 FMRQGYORELLYQREDSFSAFNGYDPSGSTWLSAFVLRCP-LEADPYIDIDONVLRHTY 1014
Db 1031 QIVTGAQOVYKADHSAFTN--RASSMLTAYVVKVFAMAQWAGISHEIICGGV 1088
QY 1015 TWL-KHQKNGEFWDPGRVIHSELOG---GNKSPVTLTAYIVTSLGYR-----KYQPM 1066
Db 1089 RWILNRPQPDGAFKFNAPVLSGTMOGGIQAEEVYLTAFILVALLESKTIENDVNSL 1148
QY 1067 D--VQSIHPLSEFSGISDNVTALITVALSSVGSPPKAKALNMLTWRAEQEGMQWF 1124
Db 1149 DSSIKATNVLKKYK-LQRPYTTALTAYALA-----AAQNLNDRVLMMASTGRDH 1201
QY 1125 VSSEKLSQSWQPRSLDIEVAAYALLSHFLQFQTSBGIPIMRWLSQRNSLGGFASTQPT 1184
Db 1202 -----BEYNARHTNIEGTSYALLALLKMKKFDQTPVIRWLTQDNYFETYGTQAT 1253
QY 1185 TVALKALSEFAALMNTER-TNIOVTVTGSPSPPL-----AVQVP--MAVNI 1228
Db 1254 VMAFQALAEYIOMPHKQNLNLTIELDPREVPIRYRYNENALLARTVETKLNQDITV 1313
QY 1229 SANGFGFAICQLNVNKNVKNASGSSRRRRSITQOEAFDLQVAVKENKDDLNHVD-----L 1282
Db 1314 TASDGGKATWILTFYNAOL---QEKANVCNK--FHLNVSE--NIHLNANGAKGALM 1365
QY 1283 NVCTSFSGPGRSGMALMEVNLISGMVVPSEAL-----LSETVKVVEYDHGKLN-----L 1332
Db 1366 KICTRYLGEVDSTMTIDISMLTGLFPAEDLTRLKSGVDYRISRYEVDNNMAQKAVAVII 1425
QY 1333 YLDSVNETO-FCVNIIPAVRNFKYSNTQDASVTVDYEPERQAVRSYNSEVKLSSCDLCS 1391
Db 1426 YLNKVSSEDECHLPKILKHFEVGFIOPGSVKVSYYNLDKCTKYHHPDKGTGLLNKIC 1485
QY 1392 DVQGCRCPCDAGSGSH-----HSSVIFIFCFKLLYPM 1425
Db 1486 IGNVCRCAGETCSLSNEQERIDVPLQIERACETNVDYVYTKLLRIEE 1533

RESULT 12

US-09-017-947-35

; Sequence 35, Application US/09017947
; Patent No. 6303754
; GENERAL INFORMATION:
; APPLICANT: VOGEL, CARL-WILHELM
; APPLICANT: BREDEHORST, REINHORST
; APPLICANT: KOCK, MICHAEL
; APPLICANT: FRITZINGER, DAVID
; TITLE OF INVENTION: RECOMBINANT PROCVF
; NUMBER OF SEQUENCES: 39
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: OBLON, SPIVAK, MCCLELLAND, MAIER & NEUSTADT,
; ADDRESSEE: P.C.
; STREET: 1755 S. JEFFERSON DAVIS HIGHWAY
; CITY: ARLINGTON
; STATE: VA
; COUNTRY: USA
; ZIP: 22202
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent in Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/017,947
; FILING DATE:
; CLASSIFICATION:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/662,227
; FILING DATE: 14-JUN-1996
; ATTORNEY/AGENT INFORMATION:
; NAME: OBLON, NORMAN F.
; REGISTRATION NUMBER: 24,618
; REFERENCE/DOCKET NUMBER: 1126-0107-0X
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 703-413-3000
; TELEFAX: 703-413-2220
; INFORMATION FOR SEQ ID NO: 35:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 1648 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; US-09-017-947-35

Query Match 12.0%; Score 880; DB 4; Length 1648;
Best Local Similarity 22.7%; Pred. No. 8.2e-64;
Matches 365; Conservative 295; Mismatches 664; Indels 284; Gaps 59;

QY 18 AALAV-----APGREFLVAPGIIRPGNVITIGVELL-EHCPSQVTVKA---ELLKTAS 67
Db 10 AALLIGPGSGHAGLYTLITPAVIRDTTEEQILVEAHGDSPTKQLDIFVHDFPRKQKTLF 69
QY 68 NLTVSVLEAEGVFKSGFKTLTLPFLPNSADEIYELRVTRGTQDEILFNSNTRLSPTK 127
Db 70 QTRVDMNPAGMLVT---PTIEIPAKEVSTDSRQNVVQVTVGPQVRLEKWLVSQSS 126
QY 128 RISVFIQTDKALYKPKQEVKERVITLPSDFPKYTSNLILI--KDKPSNLIQWLQQSD 185
Db 127 --FLFIQTDKGIYTPGSPVLYRVFSM--DHTSKONKTVIVEFQTPPEGILVS---SNSVD 179
QY 186 LGVISTKTPQLSSHTILGDWSI--QVQVNDQTYQSFQVSEYVLKPKFVLTQTP---LYCS 240
Db 180 LNFF-WPYNLPDLVSLGTWRIVAKYHSPENYATFVDRKYVLPSEFVRLQSEKFFYID 238
QY 241 MNSKHLNNTIATKYGKPVKGVDTLTLPLSPFGKKNI-----TKTFKINGSANFSND 296
Db 239 GN-ENFHVSIATARYLYGEEVEG-VAFVLFGVKIDAKKSI PDSLTRIPIDGDGKATLKR 296
QY 297 EEMKQVMDSSNGLSEYLDLSSPGPVEILTVTESVTGSRNVSTNVPFKQDHYIIIEFFDY 356
Db 297 DTFRSRFFNLNELYGHTLYAS-----VTVMTEGSDXVVTQSGIHIVASPIQHETKT 350

Db 127 --FLFIQTDKGIYTPGSPVLYRVFSM--DHHTSKNNKTIVIEFQPEGILVS---SNSVD 179
QY 186 LGWISKTFLSSHPILGDHSI--QOVNDQTYQSPQSEYVLPKFEVTLQTP---LYCS 240
Db 180 LNFF-WPYNLPDLVSGTWRIVAKYEHSPENYATYFVDRKYLPSPFVRLQSPKFFYID 238
QY 241 MNSKHLNGITAKYTYGPKVKGVDVTLFPLFSWGKKKI-----TKTEKINGSANFSND 296
Db 239 GN-ENFHVSTIARYLYGEEVEG-VAFVFGVKIDDAKKSIPDLSLFEIPIIDGGRATLKR 296
QY 297 EEMKVNDSNGLSEYLDLSSPGPBEILTVTESVTGIGSRNVSTWVFFKQHDYIIEFPDY 356
Db 297 DTFRSFPNLNELVGHTLVAS-----VTVMTESGSDVVTQSGIHIVASPYQHFTKT 350
QY 357 TTVLKSNAFTAVKVYTRADGNQLTLERNNVWIVTQRTNYTEYWSGNSGNQKMEAVQ 416
Db 351 PKYFKGMPYELTYVYNDGSPA-----AHVPVSEAF-----HSMGTIISDGT 396
QY 417 KINYVPOSGTKFIEPFILEDSELOKAYFTLGSKSSVAHSLFKSPKTYIQLKTRDEN 476
Db 397 KLILNPLNAQ---SLFITVTRTHGDLPRERQATKSMTAIAYTQGGSGNYLHVAITSTE 453
QY 477 IKVGS--PELVVSGN---KALKELSYMVVRGQLVAVGKONS-----TM-TSLTPE 522
Db 454 IRPGDNLPNFNVKGNANSLKQIKYFYILNLNKGKIFRVGRPRRDQGNLVTMNLHTPD 513
QY 523 NSWTPKACVIVYIEDGBIISDLVKIPVQ-----LVFK--NKIKLYWSKVKAEPSEKV 574
Db 514 LIPSPP--FVAYYQVGNNEIVADSVWVDKTCMGTLVVKGDNLIQMPGAAMKILEGDF 571
QY 575 SURISVTQDSIVGIVAVDKSVNLNANSDITWENVVHELELYNTGYILGMPFNFAVPO 634
Db 572 GAR-----VGLVAVDKAVYVLNDKYKISQAKIWDITIEKDFGCTAGSQNNLGVPE 622
QY 635 ECLGLWLTDAUL-TKD-----649
Db 623 DAGLALTTSTNLNKTORSAAKCPQANRRRRSVLLSDNSAKAEAFQDDLRKCCEDVM 682
QY 650 -----YIDGYD--NABYAEFRM--BENE-CHIVD 674
Db 683 HENPMGYTCEKRAKYIQEGDACKAFLPCCRYIKGVRENQRESELEFLARDNEDGFAD 742
QY 675 IHDPSLGSFPHVKHPEPEWML-----DTWGYRIYQEFVETVPDSTSWATGCVIS 728
Db 743 SOLIS-----RSDPFWMLWTKDITTEPNSQGISKTMFYLRDSITTVWVLAVFT 795
QY 729 EDLGLGLTTPVELQAFQFFIFLNLFPYVIRGEEPALEITIFNYLKDATEYKVIIEKSD 788
Db 796 PTGKI-CVAEPYRVMKVFFIDLQMPYSVVKNEQVEIRAILHNVYVEDIYVRVELLYNP 854
QY 789 KFDILMTSEINATGHOQLLVPSEDGATVLPFIRPTHG--EIPITVTALSPTASDAVT 846
Db 855 AF-----CSASTKGQRYRQPPKALSSRAVPPFVIVPELQGLHDVEIKASVQBALWSDGVR 910
QY 847 QMLVKAEGTEKYSQSILDLTDNRLOST-----LKTLSFPDNTVTGSEVRQITAI 900
Db 911 KCLKVPEGVQKSIIVTVKLDPRKGVGTQLEVIKARKLDRDVPDETEIKIILQGPV 970
QY 901 GDVLGPSING--IASIIRPYGGEQGNINFPANI---YILDYLTKKKOLTNLKEKALS 955
Db 971 AQIENSIDGSKNLHLIITPSGGEQNMIRMAAPVIATYVLDTEQWETLGINRRTEAVN 1030
QY 956 FMEQGYQRELLYQREGSFAFNYPDPSGTWLSAFVLCF-LEADPYIDIDQNVLHRY 1014
Db 1031 QIVTGAQQWYKKAHSHSAFTN--RASSMLTAYVVKVAFAMAKWAGISHEIICGV 1088
QY 1015 TWL-KGHQKSNGEFWDPGRYVHSELOQ---GNKSPVTLTAYIVTSLLYR-----RYQPM 1066
Db 1089 RWLILNRQPDGAFKENAPVLSGTMGGIGQAEVEVYLTAFILVALLESKTCINDVNSL 1148
QY 1067 D--VQESIHFLESEFGRGSDNYTLALITYALSSVGSPPAKALNMLTWRAEQEGMQPW 1124

Db 1149 DSIKATNYLLKKYK-LQRPYTTALTAYALA-----AADQLNDRDVLMAASTGRDHW 1201
QY 1125 VSSSKLSDSQWPSRLDIEVAVALLSHFLOFQFOTSEGIPIRWLSRORNSILGGFASTODT 1184
Db 1202 -----EENATHNIEGTSYALLALLKMKKFDQGPVRLWLTDFONFYGETYGOQAT 1253
QY 1185 TVALKALSEFAALMNTER-TNIQVTVTPGSPSPSL-----AVQV---MAVNI 1228
Db 1254 VMAFCAAEYBIQMPHTKDLNLDITIELPDREVPYRINYENALLARTVETKLNQDITV 1313
QY 1229 SANGFGPAICOLNVVNVKASGSRRRSTONQAEFOLDVAVKENKDDLHVD-----L 1282
Db 1314 TAGDGKATMTILTYNAQL-----OEKANVCNK--FHLNVSE--NIHLNMGAKGALML 1365
QY 1283 NVCTSFSGPGRSGMALMEVLLSGFMVPSAIS-----LSETVKKVEYDHGKLN-----L 1332
Db 1366 KICRYLGEVDSTWITIDISMLTGFLPDAEDLTLSKGVDRYISRYEVDNMAQKVAVII 1425
QY 1333 YLDSVNETQ-PCVNIPAVRNFKVNTODASVISVDYIEPRQAVRSYNSSEVLSDDLCS 1391
Db 1426 YLNKVSHEDECLHPKILKHFEVGFIOGSKVYSYNNLDEKCTKTFYHPDKGTGLLNKIC 1485
QY 1392 DVQCRPCEDGASGSH-----HSSVIFFCFLYFME 1425
Db 1486 IGNVCRAGETCSSLNQERIDVPLQIEKACETNVVDVYVTKLRIEE 1533

RESULT 14

US-08-447-411-76
; Sequence 76, Application US/08447411
; Patent No. 5773243
; GENERAL INFORMATION:
; APPLICANT: FRITZINGER, DAVID C.
; APPLICANT: BREDEHORST, REINEARD
; APPLICANT: VOGEL, CARL-WILHELM
; TITLE OF INVENTION: DNA ENCODING COBRA C3, CVF1, AND CVF2
; NUMBER OF SEQUENCES: 81
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: OCLON, SPIVAK, MCCLELLAND, MAIER & NEUSTADT,
; STREET: 1755 S. Jefferson Davis Highway, Suite 400
; CITY: Arlington
; STATE: Virginia
; COUNTRY: U.S.A.
; ZIP: 22202
; COMPUTER-READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/447,411
; FILING DATE:
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/043,747
; FILING DATE: 07-APR-1993
; ATTORNEY/AGENT INFORMATION:
; NAME: OCLON, No. 5773243man F.
; REGISTRATION NUMBER: 24,618
; REFERENCE/DOCKET NUMBER: 1126-101-0
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (703) 413-3000
; TELEFAX: (703) 413-2220
; TELEX: 248855 OPAT UR
; INFORMATION FOR SEQ ID NO: 76:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 1333 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
US-08-447-411-76

Query Match 10.5%; Score 768.5; DB 1; Length 1333;
Best Local Similarity 24.4%; Pred. No. 1.2e-54;
Matches 301; Conservative 208; Mismatches 477; Indels 247; Gaps 45;

QY 349 YIIFFDYTTVLKPSLNFTATVTRADGNQLTLEERNVIVITQRTNYTWYSGNSG 408
DB 22 YQIYFTKPKYKFGMPYELTVVTRPDGSPA-----HVPVSEAHSE-----G 67

QY 409 NQKWEAVQKINYTPQSGTFKIEFFILEDSELOLKAYFLGSKSSVAHSLFKSPSTYI 468
DB 68 TTLDGDTAKFLNTPQNAQ---SLPITVTRNHGDLPRERQAISMTATAYQTQGGSGNYL 124

QY 469 QLKTRDENIKVGS--PELVVSGN---KRLKELSYMVVSRGOLVAVGKQNS-----T 515
DB 125 HVAITSTEIKPGDNLPNFNVNRGNANSLNQIKYFTYLLNKGKIFKVGQHRGDGENLYT 184

QY 516 M-FSLTPENSWTPKACVIVYIIEDDGRIISDVULKIPVQ-----LVFK-----NKIKLY 562
DB 185 MNLHITPD--LIPSRFVAYTYQGNNEIVADSVYVDVTKDTCMTLVVKGATSRDRNQW- 241

QY 563 WSKVKAPESEKSLRISVTPDQSIQVIGVADKSVNLMNASNDITMENVVHELELYNTGY 622
DB 242 -----PGAAKIKLE-GDQGAWIGLVAVDKAYVINDKYKISQAKIWDITIEKSDFGCT 293

QY 623 LGHFMNSFAVBOCGWLVTLDANLT-----DNTMGYRIYQBEFVTPVPSITSW 720
DB 294 AGSGQNNLGVFEDAGLATLTSTNLTKQSAKCPQANRRRRSSVLLDSDNASKAAQFQ 353

QY 648 -----KDYIDGVND-----AEVAERFMENEG-----HIV-----673
DB 354 DQBLRKCCEGDMHENPMNGHTCEKREKYOIGDACKAAFLCCHYKIGIQDDNKRSELEP 413

QY 674 ---DIDHFSGSPHV--RKHFPTIWL-----DTNMGYRIYQBEFVTPVPSITSW 720
DB 414 ARGDFEDDLFEGNITSRSPFPPSWLWMLQELSEHPNSKGIKVPFY--LRDSITW 470

QY 721 VATGVISEDLGLGLTT-----PVELQAFOPFIPLNLYSVIRGEBEPALEITIFY 773
DB 471 -----ELLAVGLSPKIGICVAEPYEITWMDFFIDQLPYSVYVKNQKIRAVLYNY 522

QY 774 LKQATEVKVIEKSDFDILMTSEINATGHOOTLLVPSEGDATVLFIRPHTLG--EIP 831
DB 523 ADKDIYVURVELLSPAPCSASTEQ-----RYRQLPIKALSRAVSVFVIPLEQGLHVE 578

QY 832 ITVTALSPASDAVQMLKABEGIEKYSQSILLDLTDNRLOST-----LKTLSFSP 885
DB 579 VTASVQELMSDGVKKLKVVPGEWKSIVTIELDPHTKIGIGTQVELVKAANKLNDVFP 638

QY 886 PNTVTGSEYQITAGDVLGSPING--LASLIRMPYCGGQNNINF-APNI--YILDVLT 940
DB 639 DTEIETKITIQDPVAQTIENSIDGSKNLNLIITPFCGGEQNMRTAPVIATYLLDTQ 998

QY 941 KKKQLTDNLKELKALSPMROGYQRELLYQREDGFSFAGNYPDPSGTWLSAFVLRCP-LEA 999
DB 699 QWETLGINRRTEAVNQIMTQYAOOLVYKADHSYAFTN--SASSSWLTAYVYVKIPALAA 756

QY 1000 DPVIDIDQNLHRTIYWL--KGHOKSNGEPWDPGRVTHSELOGNKPV--TLTAVITS 1055
DB 757 KIVKINDINHEVCGMRWLILNRQTDGVFRENAPVLFGTMQGGIQGAEPESLUTAFILVA 816

QY 1056 LLGKRYQPNIDVQESIHLESFBSRQ-----ISDNYTLALITYALS SVGSPKAK 1105
DB 817 LLSRSRI-----CNAYINILDSISKATDVLKKYKELQRPYTLTAYALA-----AA 865

QY 1106 EALNMLTWABEQCGMGQFVSSSEKSDSWQPSRLDIEVNAAYALLSHFQFQTSIGIPM 1165
DB 866 ERLNDRDLVMAASTGRNRWEPNA-----HTHNIECTSYALLALLKKYKFEAGPVV 917

QY 1166 RWLSRQNSLGGPASTODTTLVALKALSEFAALMNTER-TNIOVTVTGSPSPS-----1217
DB 918 QWLIDQYVGGTYGQTOATVWMTQALAEYEQPTHKDLNLDITIELDPREPIRVINY 977

QY 1218 ----LAVVQPMVNV-----ISANGFGFAICOLNVVNVKASGSSRRRRSTONQAEFLDVA 1269

DB 978 ENALLAQVETKLNEDFTVSASGDGKATMITLITVYNAQL-----REDANVCNK--FHLDSV 1031

QY 1270 V-----KENKDDLNVLDLVNCTSPSGPGRSGMALMEYNLLSGFVWPSEALS-LSETVK 1321

DB 1032 VENVQLMLKEAKGAKGALKIKICTRYLGEVDSTWTTIIVDSMLTGFVDPDTEDLRLSKGVD 1091

QY 1322 K-----VEYDH-----GKLNLYLDSVNETQ--FCVNIIPAVRNFKVSNTQDASVIVDYEPR 1371

DB 1092 RYISWFELNNNAQMGTVIYLDKVKSHSEDECLHFKILKEHFEVGFIOGSKVSVYNYLD 1151

QY 1372 QRAVRSNVSEKVLSSCDLSDVQGCRCEDGAS 1404

DB 1152 EKCTKIYHPDEATGLNLNKICVGNVCRCAETCS 1184

RESULT 15
US-08-662-227-34
; Sequence 34, Application US/08662227
; Patent No. 5922320
; GENERAL INFORMATION:
; APPLICANT: VOGEL, CARL-WILHELM
; APPLICANT: BREDEHORST, REINHORST
; APPLICANT: KOCK, MICHAEL
; APPLICANT: FRITZINGER, DAVID
; TITLE OF INVENTION: RECOMBINANT PROCVF
; NUMBER OF SEQUENCES: 39
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: OBLON, SPIVAK, MCCLELLAND, MAIER & NEUSTADT,
; STREET: 1755 S. JEFFERSON DAVIS HIGHWAY
; CITY: ARLINGTON
; STATE: VA
; COUNTRY: USA
; ZIP: 22202
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patentin Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/662,227
; FILING DATE: 14-JUN-1996
; CLASSIFICATION: 530
; ATTORNEY/AGENT INFORMATION:
; NAME: OBLON, NORMAN F.
; REGISTRATION NUMBER: 24,618
; REFERENCE/DOCKET NUMBER: 1126-0107-OX
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 703-413-3000
; TELEFAX: 703-413-2220
; INFORMATION FOR SEQ ID NO: 34:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 1333 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: protein
US-08-662-227-34

Query Match 10.3%; Score 758.5; DB 2; Length 1333;
Best Local Similarity 24.4%; Pred. No. 8.2e-54;
Matches 301; Conservative 208; Mismatches 477; Indels 247; Gaps 46;

QY 349 YIIFFDYTTVLKPSLNFTATVKTADGNQLTLEERNVIVITQRTNYTWYSGNSG 408
DB 22 YQIYFTKPKYKFGMPYELTVVTRPDGSPA-----HVPVSEAHSE-----G 67

QY 409 NQKWEAVQKINYTPQSGTFKIEFFILEDSELOLKAYFLGSKSSVAHSLFKSPSTYI 468
DB 68 TTLDGDTAKFLNTPQNAQ---SLPITVTRNHGDLPRERQAISMTATAYQTQGGSGNYL 124

QY 469 QLKTRDENIKVGS--PELVVSGN---KRLKELSYMVVSRGOLVAVGKQNS-----TM 516

Db 125 HVAITEIKPGNLPNPNVRNANSLNCOIKFYTLILNKGKIFKVGROHGRDGNLVTM 184
QY 517 -FSLTPENSWTPKACVIVVYIEDGFI-ISDVLKIPVQ-----LVFK-----NKIKLY 562
Db 185 NLHITPD--LIPSFREVAIVYQVGNNEIEVADSVWVDKDTCMGTLVKGATSRDNRQIOW- 241
QY 563 WSKVKAEBSEKYSRLRSVTPQDSIVGIVAVDKSVNLMNASNDITMENVVEHELELYNTGY 622
Db 242 -----PGAAMKIKLE-GDPAWKILE-GDPAWKILE-GDPAWKILE-GDPAWKILE-GDPAWKILE- 293
QY 623 LGMFMNSFAVFOECGLVWLTDANLT----- 647
Db 294 AGSGQNNLGVFEDAGLALTTSTNLNTKORSAKQPOANRRRRSSVLLDLSNASKAAQFQ 353
QY 648 -----KDYIDGVYDN-----AEYAEFMEENEG-----HIV----- 673
Db 354 DDLRKRCCEDGHEHNPWGHTCEKREYIOGDAKAAFLCCHYIKGIODDNKRSEFL 413
QY 674 ---DIHDFSLSGSPHV-RKHFPETIWL-----DTNMGYRIYQEEVTVPDPSITSW 720
Db 414 ARSDFEDDLFEGENIISRSDFPESWLMWMEQLSEHNSKGISKIVPFY--LRDSITW 470
QY 721 VATGFVISDGLGLTFT-----PVELQAFQPFIFLNPYSVIRGEFALBITIFY 773
Db 471 -----ELLAVGLSPTKIGICVAEPEYITWKFIDQLPYSVVVKNQKIRAVLNY 522
QY 774 LKDATEVKVILIEKSKDFDILMTSSEINATCHQOTLLVPSEGDATVLPFIRPTHLG--BIP 831
Db 523 AKDIYVRVELLYSPAFCSASTESQ-----RYREQLPIKALSRASVFIIVPLEQGLHVE 578
QY 832 ITVTALSPASDAVTOMLVKAERGIEKYSQSILDLTDNRLOST-----LKTLSFSFP 885
Db 579 VTASVQGLMSDGVKKLKVVPBGWKSIVTIELDPHTKGIGTQVELVANKANDRVP 638
QY 886 PNTVTSERVOITAIGDVLGPSING--LASLRMPYGCGEONMIF-APNI--YILDYLT 940
Db 639 DTEIETKITIQGDPVACTIENSIDGSKLNHLIITPFGCGEONMIRMTAPVIATYYLDTTQ 698
QY 941 KKKQLTDNLKEKALSPMRQYQRELLYQREDGSFSAFNGVDPSPGTSWLSAFVLRGF-LEA 999
Db 699 QWETLGINRTEAVNQIMTGAYQQLVYKKADHSYAFTN--SASSSWLTAYVVKIFALAA 756
QY 1000 DPYIDIDQNVLHRTYTWL-KGHQKNGEPWDPGRVHSEHQNGKSPV--TLTAYIVTS 1055
Db 757 KIVKIDINHEIVCGMRWLILNQRDTDGVFRENAPVLFGTWQGIQGAEPESLITAFILVA 816
QY 1056 LLGYRYQPNIDVQESIHLESEFSRG-----ISDNYTLALITVALSSVGSPPAK 1105
Db 817 LLESRI-----CNVINILDSISIKATDYLKKYKLOPYYTALTAYALA-----AA 865
QY 1106 EALNMLTWRAEQBGMCQFWSSSKLSDSQPRSLDIEVAAYALLSHFLQFOTSEGIPTM 1165
Db 866 ERLNDRVLMAASTGRNWEENPNA-----HTHNIETSVALLALLKMKKFVEAGPV 917
QY 1166 RWLSRORNSLGGPASTQDITVALKALSEFAALMNTER-TNIQVTVGSPSP----- 1217
Db 918 QWLIDQOYGGTYGQTCATVMFQALAEYEQMPTHKOLNLDITIELPREVPIRYNY 977
QY 1218 ----LAVQPMAN-----ISANGFPAICOLNVVNVKASGSSRRRSIQNOEAPDLVA 1269
Db 978 ENALLAQTVETKLNEDFTVSASGCGKATWILTIVYNAQL-----REDANVCNK--FHLDS 1031
QY 1270 V-----KENKDDLHNDLVNCTSPSGRSGMALMEVNLISGFMVPSA-S-LSETVK 1321
Db 1032 VENVQLNKEAKGALKKICTRYLGEVDSNTIIDVSMLTGFPVPTEDLTRLSKGD 1091
QY 1322 K-----VEYDH-----GKLNLYLDSVNETO-FCVNIPEAVNEKVSNTQDASVSDVYEP 1371
Db 1092 RYISMEIINNMAQKQTVIYLDKSHSEDECLHFKILHFEVGFQPGSVKVYSYNDL 1151
QY 1372 ROAVRSYNSEVKLSSCDLSDVOGCRPCEDGAS 1404

Db 1152 BKCTKIYHPDEATGLLNKICVGNVCRCAEETCS 1184

Search completed: August 10, 2004, 19:34:42
Job time : 34 secs

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Result No.	Score	Query Match	Length	DB	ID	Description
1	2584.6	60.3	3033	9	US-09-8933-381-1810	Sequence 1810, App
2	1969.4	45.9	2273	16	US-10-108-260A-953	Sequence 953, App
3	1690.8	39.4	1880	13	US-10-112-944-160	Sequence 160, App
4	1017	23.7	1448	16	US-10-264-377-1040	Sequence 1040, App
5	975.4	22.8	1459	13	US-10-276-774-601	Sequence 601, App
6	730.8	17.0	1300	15	US-10-133-013-223	Sequence 223, App
7	541.6	12.6	875	10	US-09-820-649-48	Sequence 48, Appl
8	541.6	12.6	875	15	US-10-160-162-48	Sequence 48, Appl
9	525	12.2	821	13	US-10-211-462-208	Sequence 208, App
10	497.4	11.6	520	13	US-10-085-783A-45412	Sequence 45412, A
11	497.4	11.6	520	16	US-10-242-535A-45412	Sequence 45412, A
12	334.8	7.8	499	13	US-10-085-783A-29628	Sequence 29628, A
13	334.8	7.8	499	16	US-10-242-535A-29628	Sequence 29628, A
14	297.2	6.9	303	13	US-10-085-783A-46128	Sequence 46128, A

186 ACAATGAAATGTGGTCCATGAGTTGGAACTTTATAACACAGGATTAATTTAGGCATG 245
1876 TTCAATGAATCTTTTTCAGTCTTTTCAGGAATGGACTCTGGGTATTTGACAGATCAAAAC 1935
246 TTCAATGAATCTTTTTCAGTCTTTTCAGGAATGGACTCTGGGTATTTGACAGATCAAAAC 305
1936 CTCACGAAGATTAATTAATGATGTTTATGACAATGCGAGATATGCTGAGAGGTTTATG 1995
306 CTCACGAAGATTAATTAATGATGTTTATGACAATGCGAGATATGCTGAGAGGTTTATG 365
1996 GAGGAAATCAAGGACATATTTGATGATTTTCATGACTTTTCTTGGGTAGCAGTCCACAT 2055
366 GAGGAAATCAAGGACATATTTGATGATTTTCATGACTTTTCTTGGGTAGCAGTCCACAT 425
2056 GTCGGAAGCATTTTCCAGAGACTTGGATTTGGCTAGACACCAACATGGGTTACAGGATT 2115
426 GTCGGAAGCATTTTCCAGAGACTTGGATTTGGCTAGACACCAACATGGGTTACAGGATT 485
2116 TACCAAGATTTTCAAGTAACTGTACCTGATTTCTATCACTTTCTTGGGTGCTACTGTTTT 2175
486 TACCAAGATTTTGAAGTAACTGTACCTGATTTCTATCACTTTCTTGGGTGCTACTGTTTT 545
2176 GTGATCTCTGAGGACCTGGTCTTGGACTAACTACTCCAGTGGAGTCCAAAGCCTTC 2235
546 GTGATCTCTGAGGACCTGGTCTTGGACTAACTACTCCAGTGGAGTCCAAAGCCTTC 605
2236 CAACCAATTTTCAATTTTGAATCTTCCCTACTCTGTTATCAGAGTGAAGATTTGCT 2295
606 CAACCAATTTTCAATTTTGAATCTTCCCTACTCTGTTATCAGAGTGAAGATTTGCT 665
2296 TTGGAATACTATATTTCAATTTTGAAGTAACTACTCCAGTGGAGTCCAAAGCCTTC 2355
666 TTGGAATACTATATTTCAATTTTGAAGTAACTACTCCAGTGGAGTCCAAAGCCTTC 725
2356 AAAAGTGAACAAATTTGATATTTCAATTTTGAAGTAACTACTCCAGTGGAGTCCAAAGCCTTC 2415
726 AAAAGTGAACAAATTTGATATTTCAATTTTGAAGTAACTACTCCAGTGGAGTCCAAAGCCTTC 785
2416 CAGACCTCTCTGTTCCAGTGAAGTGGGCACTGTTCTTTTCCCATCAGGCCAACA 2475
786 CAGACCTCTCTGTTCCAGTGAAGTGGGCACTGTTCTTTTCCCATCAGGCCAACA 845
2476 CATCTGGAGAAATTCCTATCAGTCAAGTCAAGTCTTTTCCCATCAGGCCAACA 2535
846 CATCTGGAGAAATTCCTATCAGTCAAGTCAAGTCTTTTCCCATCAGGCCAACA 905
2536 ACCAGATGATTTAGTAAAGGCTGAAGGATGAAGGATTAATTTCAATTTCAATTTCA 2595
906 ACCAGATGATTTAGTAAAGGCTGAAGGATGAAGGATTAATTTCAATTTCAATTTCA 965
2596 TTAGACTTGACTGACATAGGCTACAGTACCTCGAAATCTTTGAGTTTCTCATTTCT 2655
966 TTAGACTTGACTGACATAGGCTACAGTACCTCGAAATCTTTGAGTTTCTCATTTCT 1025
2656 CTTAATACAGTGAAGTGAAGGATTTGATGATTTGATGATTTGATGATTTGATGATTT 2715
1026 CTTAATACAGTGAAGTGAAGGATTTGATGATTTGATGATTTGATGATTTGATGATTT 1085
2716 CTTTCAATCAATGGCTTACGATTTGATGATTTGATGATTTGATGATTTGATGATTT 2775
1086 CTTTCAATCAATGGCTTACGATTTGATGATTTGATGATTTGATGATTTGATGATTT 1145
2776 ATGATAAATTTTGTCCAAATATTTTACATTTTGGATTTTCTGATTTTAAAGAAACAACTG 2835
1146 ATGATAAATTTTGTCCAAATATTTTACATTTTGGATTTTCTGATTTTAAAGAAACAACTG 1205
2836 ACAGATAATTTTGAAGAAAGGCTTTTCAATTTTATGAGGCAAGTTTACAGAGAGACTT 2895
1206 ACAGATAATTTTGAAGAAAGGCTTTTCAATTTTATGAGGCAAGTTTACAGAGAGACTT 1265
2896 CTTCTACAGAGGAAAGTGGCTCTTTTCAAGTCTTTTGGAAATTAAGCCCTTTCTGGAGC 2955

1266 CTCTATCAGAGGAGATGGCTCTTTTCAGTGTCTTTTGGGAATTTATGACCCCTTCTGGGAGC 1325
2956 ACTTGGTGTGACGCTTTTAAAGATGTTTCTTGAAGCCGATCTTACATAGATATT 3015
1326 ACTTGGTGTGACGCTTTTAAAGATGTTTCTTGAAGCCGATCTTACATAGATATT 1385
3016 GATCAGATGTTTACACAGAAATACATCTTGGCTTAAAGGACATCAGAAATCCAAAGGT 3075
1386 GATCAGATGTTTACACAGAAATACATCTTGGCTTAAAGGACATCAGAAATCCAAAGGT 1445
3076 GAAATTTTGGGATCCAGGAAGATGATTTATAGTGGCTTCAAGGTGGCAATAAAGTCCA 3135
1446 GAAATTTTGGGATCCAGGAAGATGATTTATAGTGGCTTCAAGGTGGCAATAAAGTCCA 1505
3136 GTRACACTTACAGCCTATATTGTAATCTTCTCTGGATATAGAAAGTATCAGCCTAAC 3195
1506 GTAACTTACAGCCTATATTGTAATCTTCTCTGGATATAGAAAGTATCAGCCTAAC 1565
3196 ATTGATGTGAAGAGTCTATCCATTTTGGAGTCTGAATTCAGTAGAGGAATTTCAAGC 3255
1566 ATTGATGTGAAGAGTCTATCCATTTTGGAGTCTGAATTCAGTAGAGGAATTTCAAGC 1625
3256 AATTATATCTAGCCCTTATACTTATGATTTGATTCATCAGTGGGAGTCTTAAAGGAG 3315
1626 AATTATATCTAGCCCTTATACTTATGATTTGATTCATCAGTGGGAGTCTTAAAGGAG 1685
3316 GAAGCTTTGAATATGCTGACTTGGAGAGCAGAAACAAAGGTGGCATGCAATTTCTGGGTG 3375
1686 GAAGCTTTGAATATGCTGACTTGGAGAGCAGAAACAAAGGTGGCATGCAATTTCTGGGTG 1745
3376 TCATCAGAGTCCAAACCTTCTGACTCTGGAGCCAGCTCTTCAAGTATGAAAGTGA 3435
1746 TCATCAGAGTCCAAACCTTCTGACTCTGGAGCCAGCTCTTCAAGTATGAAAGTGA 1805
3436 GCCTATCAGTCTCTCAGACTTCTTCAATTTTCAAGTATGAAAGTGA 3495
1806 GCCTATGAGTCTCTCAGACTTCTTCAATTTTCAAGTATGAAAGTGA 1865
3496 AGGTGGCTTAAAGGCTCTGCTGATTTTGAAGTATGAAAGTGA 3555
1866 AGGTGGCTTAAAGGCTCTGCTGATTTTGAAGTATGAAAGTGA 1925
3556 GTGCTTTTAAAGGCTCTGCTGATTTTGAAGTATGAAAGTGA 3615
1926 GTGCTTTTAAAGGCTCTGCTGATTTTGAAGTATGAAAGTGA 1985
3616 CAAGTGAAGGCTGAGGCGCTTAGCTCAACCAAGTCTTCTGAAAGTCTTCTGATTTGACACAC 2045
1986 CAAGTGAAGGCTGAGGCGCTTAGCTCAACCAAGTCTTCTGAAAGTCTTCTGATTTGACACAC 2045
3652 CTTGCTGTGTACAGCAATGGCAGTATTAATTT 3684
2046 AACCGCTTACTCTTACAGCAGAGCTTGTCTGATCAGCAATGGCAGTATTAATTT 2105
3685 TCCGCAATGTTTGTGATTTGCTGATTTGCTGATTTGCTGATTTGCTGATTTGCTGATTT 3744
2106 TCCGCAATGTTTGTGATTTGCTGATTTGCTGATTTGCTGATTTGCTGATTTGCTGATTT 2165
3745 TCTGGGTCTTGAAGAGCAAGATTTATCCAAATCAAGAGCCTTTGATTTGATTTGATTT 3804
2166 TCTGGGTCTTGAAGAGCAAGATTTATCCAAATCAAGAGCCTTTGATTTGATTTGATTT 2225
3805 GCTGTAAAGAAATTAAGATGATTTCAATCATGTTGATTTGATTTGATTTGATTTGATTT 3864
2226 GCTGTAAAGAAATTAAGATGATTTCAATCATGTTGATTTGATTTGATTTGATTTGATTT 2285
3865 TCGGCCCCGGGTAGGAGTGGCTCTTATGGAAGTAACTTAACTTAACTTAACTTAACTTAACT 3924
2286 TCGGCCCCGGGTAGGAGTGGCTCTTATGGAAGTAACTTAACTTAACTTAACTTAACTTAACT 2345
3925 GTGCTTTCAAGAGCAATTTCTTCAAGGAGCAGTGAAGAGTGAAGTGAAGTGAAGTGAAG 3984
2346 GTGCTTTCAAGAGCAATTTCTTCAAGGAGCAGTGAAGAGTGAAGTGAAGTGAAGTGAAG 2405

QY	3985	AAACTCAACCTCTATTAGATTCTGTAAATGAACCCAGTTTGTGTTAATATTCCTGCT	4044
Db	2406	AAACTCAACCTCTATTAGATTCTGTAAATGAACCCAGTTTGTGTTAATATTCCTGCT	2465
QY	4045	GTGAGAACTTTAAAGTTTCAAAATACCCAGATGCTTCAGTGCCTAGTGGATTAATAT	4104
Db	2466	GTGAGAACTTTAAAGTTTCAAAATACCCAGATGCTTCAGTGCCTAGTGGATTAATAT	2525
QY	4105	GAGCCAAAGGAGACAGCGGTGAGAAAGTTTACAACCTCTGAAAGTGAAGCTGCTCCTGTGAC	4164
Db	2526	GAGCCAAAGGAGACAGCGGTGAGAAAGTTTACAACCTCTGAAAGTGAAGCTGCTCCTGTGAC	2585
QY	4165	CTTTGAGTGAATGTCAGGCGTCCGCTCTTGTGAGAGTGGAGCTTCAGGCTCCCATCAT	4224
Db	2586	CTTTGAGTGAATGTCAGGCGTCCGCTCTTGTGAGAGTGGAGCTTCAGGCTCCCATCAT	2645
QY	4225	CACCTCTCAGTCAATTTTATTTTCTGTTTCAAGCTTCTGCTGCTTATGAACTTTGGCTG	4284
Db	2646	CACCTCTCAGTCAATTTTATTTTCTGTTTCAAGCTTCTGCTGCTTATGAACTTTGGCTG	2705
QY	4285	TGA 4287	
Db	2706	TGA 2708	
RESULT 2			
US-10-108-260A-953			
; Sequence 953, Application US/10108260A			
; Publication No. US20040005560A1			
; GENERAL INFORMATION:			
; APPLICANT: HELIX RESEARCH INSTITUTE			
; TITLE OF INVENTION: No. US20040005560A1e1 full length cdna			
; FILE REFERENCE: HI-A0106			
; CURRENT APPLICATION NUMBER: US/10/108, 260A			
; CURRENT FILING DATE: 2002-03-27			
; NUMBER OF SEQ ID NOS: 5458			
; SOFTWARE: PatentIn Ver. 2.1			
; SEQ ID NO 953			
; LENGTH: 2273			
; TYPE: DNA			
; ORGANISM: Homo sapiens			
US-10-108-260A-953			
Query Match 45.9%; Score 1969, 4; DB 16; Length 2273;			
Best Local Similarity 99.9%; Pred. No. 0;			
Matches 1970; Conservative 0; Mismatches 1; Indels 0; Gaps 0;			
QY	1	ATGCAGGCGCCACCGCTCTCTGACCGCGCCACCTCTCTGCTGTGTCACCGCGCGCTG	60
Db	66	ATGCAGGCGCCACCGCTCTCTGACCGCGCCACCTCTCTGCTGTGTCACCGCGCGCTG	125
QY	61	GCCGTGGCTCCCGGCTCCGTTTCTGTCACAGCCCGGATCATCAGGCGCGGAGGA	120
Db	126	GCCGTGGCTCCCGGCTCCGTTTCTGTCACAGCCCGGATCATCAGGCGCGGAGGA	185
QY	121	AATGTGACTATTGGGTGGAGCTTCTGGAACACTGCGCTTCACAGTGACTGTGAAGGCG	180
Db	186	AATGTGACTATTGGGTGGAGCTTCTGGAACACTGCGCTTCACAGTGACTGTGAAGGCG	245
QY	181	GAGTGTCTAAGACAGCATCAACCTCACTGTCTGTCTGTCGTAAGCAGAGAGTCTTT	240
Db	246	GAGTGTCTAAGACAGCATCAACCTCACTGTCTGTCTGTCGTAAGCAGAGAGTCTTT	305
QY	241	GAATAAGGCTCTTTAAGACACTTACTTCTTCCATCACTACTCTGAACAGTGCAGATGAG	300
Db	306	GAATAAGGCTCTTTAAGACACTTACTTCTTCCATCACTACTCTGAACAGTGCAGATGAG	365
QY	301	ATTTATGAGTACGTGTAACCGAGCGTACCGAGATGAGATTTATCTCTAATAGTACC	360
Db	366	ATTTATGAGTACGTGTAACCGAGCGTACCGAGATGAGATTTATCTCTAATAGTACC	425
QY	361	CGCTTATCATTTGAGACCAAGAGATATCTGTTCTTCAACACAGACAGGCTTATAC	420

Db	426	CGCTTATCATTTGAGACCAAGAGATATCTCTCTTCATTCACCAAGCCCTTATAC	485
QY	421	AAGCCAAAGCAAGAGTGAAGTTTGCATTTTACACTCTCTTCTCAGATTTTAAAGCCTTAC	480
Db	486	AAGCCAAAGCAAGAGTGAAGTTTGCATTTTACACTCTCTTCTCAGATTTTAAAGCCTTAC	545
QY	481	AAACCTCTTTAAACATTTCTCATTAAGGACCCCAAAATCAAAATTTGATCAACAGTGGTG	540
Db	546	AAACCTCTTTAAACATTTCTCATTAAGGACCCCAAAATCAAAATTTGATCAACAGTGGTG	605
QY	541	TCACAAACAAAGTATCTTGGAGTCAATTTCCAAAACCTTTTCAGCTATCTTCCCATCCAATA	600
Db	606	TCACAAACAAAGTATCTTGGAGTCAATTTCCAAAACCTTTTCAGCTATCTTCCCATCCAATA	665
QY	601	CTTGTGACTGCTGTCTATTCAAGTTTCAAGTGAATGACCCAGACATATTAATCAATCAATTCAG	660
Db	666	CTTGTGACTGCTGTCTATTCAAGTTTCAAGTGAATGACCCAGACATATTAATCAATCAATTCAG	725
QY	661	GTTTCAGATATGATATTAACAAAATTTGAAGTGAATTTGCAGACACCATATATATGTTCT	720
Db	726	GTTTCAGATATGATATTAACAAAATTTGAAGTGAATTTGCAGACACCATATATATGTTCT	785
QY	721	ATGAATTTCAAGCAATTTAAATGGTACCATCAACGCAAAAGTATACATATGGGAAGCCAGTG	780
Db	786	ATGAATTTCAAGCAATTTAAATGGTACCATCAACGCAAAAGTATACATATGGGAAGCCAGTG	845
QY	781	AAAGGAGACGTAAACGCTTACATTTTACCTTTTACCTTTTGGGAAAGAAAGAAATATT	840
Db	846	AAAGGAGACGTAAACGCTTACATTTTACCTTTTACCTTTTGGGAAAGAAAGAAATATT	905
QY	841	ACAAAACATTTAAGATAAATGGATCTGCAAACTTCTCTTTTAAATGATGAAGAGATGAAA	900
Db	906	ACAAAACATTTAAGATAAATGGATCTGCAAACTTCTCTTTTAAATGATGAAGAGATGAAA	965
QY	901	AATGTAATGGATTTCTCAAAATGGACTTTCTGAAATCACTGGATCTATCTTCCCTGGACCA	960
Db	966	AATGTAATGGATTTCTCAAAATGGACTTTCTGAAATCACTGGATCTATCTTCCCTGGACCA	1025
QY	961	GTAGAAATTTTAAACACAGTGCACAGATCACTTACAGTATTTTCAAGAAATGTAAGCACT	1020
Db	1026	GTAGAAATTTTAAACACAGTGCACAGATCACTTACAGTATTTTCAAGAAATGTAAGCACT	1085
QY	1021	AATGTGTTCTTCAAGCAACATGATTTACATCATTTGAGTTTCTTGTATTTACTACTCTCTTG	1080
Db	1086	AATGTGTTCTTCAAGCAACATGATTTACATCATTTGAGTTTCTTGTATTTACTACTCTCTTG	1145
QY	1081	AAGCCATCTCAACTTCAAGCCACTGTGAAGTGAAGTGAAGTGAAGTGAAGTGAAGTGAAG	1140
Db	1146	AAGCCATCTCAACTTCAAGCCACTGTGAAGTGAAGTGAAGTGAAGTGAAGTGAAGTGAAG	1205
QY	1141	ACTCTTGAAGAAAGAAAGAAATAATGTAGTCAATACAGTGACACAGAGAACTATACTGAG	1200
Db	1206	ACTCTTGAAGAAAGAAAGAAATAATGTAGTCAATACAGTGACACAGAGAACTATACTGAG	1265
QY	1201	TACTGAGCGGATCTAACAGTGGAAATCAGAAATGGAAGCTGTTTCAGAAAATAAATATAT	1260
Db	1266	TACTGAGCGGATCTAACAGTGGAAATCAGAAATGGAAGCTGTTTCAGAAAATAAATATAT	1325
QY	1261	ACTGTGCCCCCAAGTGAACCTTTTAAAGTGAATTTCCCAATCCCTGGAGGATCCAGTGAG	1320
Db	1326	ACTGTGCCCCCAAGTGAACCTTTTAAAGTGAATTTCCCAATCCCTGGAGGATCCAGTGAG	1385
QY	1321	CTACAGTTTGAAGGCTATTTCTTGTAGTAAAAAGTAGCATGGCAGTTTCATAGTCTGTTT	1380
Db	1386	CTACAGTTTGAAGGCTATTTCTTGTAGTAAAAAGTAGCATGGCAGTTTCATAGTCTGTTT	1445
QY	1381	AAGTCTCTAGTGAAGATATATCAACTAAAAACAGAGATGAAATATTAAGGTGGGA	1440
Db	1446	AAGTCTCTAGTGAAGATATATCAACTAAAAACAGAGATGAAATATTAAGGTGGGA	1505
QY	1441	TGCGCTTTTGGTGTAGTGGCAACCAACATTGAAGGAGTTAAGCTATATGTTA	1500

1506	Db	TCGCCTTTTGAGTTGGTGGTTAGTGGCAACAAACGATTGAAGGAGTTAAGCTTATGGTA	1565
1501	Qy	GTATCCAGGGGACAGTTGGTGGCTGTAGGAAAAACAAATTCACAAATGTTCTCTTTAAACA	1560
1566	Db	GTATCCAGGGGACAGTTGGTGGCTGTAGGAAAAACAAATTCACAAATGTTCTCTTTAAACA	1625
1561	Qy	CCAGAAAATCTTGGACTCCAAAAGCCTGTGTAAATCTGTATTATATTGAAGATGATGGG	1620
1626	Db	CCAGAAAATCTTGGACTCCAAAAGCCTGTGTAAATCTGTATTATATTGAAGATGATGGG	1685
1621	Qy	GAATTTATAAGTGAATGTTCTAAAAATTCCTCGTTTCAGCTGTTTAAAAATAAGATAAAG	1680
1686	Db	GAATTTATAAGTGAATGTTCTAAAAATTCCTCGTTTCAGCTGTTTAAAAATAAGATAAAG	1745
1681	Qy	CTATATTGGAGTAAAGTGAAGCTGAACCAATCTTGAGAAAGCTCTCTTTAGGATCTCTGTG	1740
1746	Db	CTATATTGGAGTAAAGTGAAGCTGAACCAATCTTGAGAAAGCTCTCTTTAGGATCTCTGTG	1805
1741	Qy	ACACAGCCTCAGCTCCATAGTTGGATTTGAGCTGTTGCACAAAAAGTGTGAATCTGATCAAT	1800
1806	Db	ACACAGCCTCAGCTCCATAGTTGGATTTGAGCTGTTGCACAAAAAGTGTGAATCTGATCAAT	1865
1801	Qy	GCCTCTAATGATATTACAAATGGAAAAATGTGGTCCATGAGTTGGAACTTTTATATACACAGGA	1860
1866	Db	GCCTCTAATGATATTACAAATGGAAAAATGTGGTCCATGAGTTGGAACTTTTATATACACAGGA	1925
1861	Qy	TATTTATTGGCGATGTTTCATGAATCTCTTTTGGCAGTCTTTTCAGAAATGTGACACTCTGGTA	1920
1926	Db	TATTTATTGGCGATGTTTCATGAATCTCTTTTGGCAGTCTTTTCAGAAATGTGACACTCTGGTA	1985
1921	Qy	TTGACAGATCCAAACCTCAGAAAGGATTATATTGATGGTGTTTATGACAAAT	1971
1986	Db	TTGACAGATCCAAACCTCAGAAAGGATTATATTGATGGTGTTTATGACAAAT	2036

RESULT 3

```

US-10-112-944-160
; Sequence 160, Application US/10112944
; Publication No. US20040048249A1
; GENERAL INFORMATION:
; APPLICANT: Tang, Y. Tom
; APPLICANT: Yang, Yunchong
; APPLICANT: Wang, Gezhi
; APPLICANT: Zhang, Jie
; APPLICANT: Ren, Feiyang
; APPLICANT: Xue, Aidong J.
; APPLICANT: Wang, Jian-Rui
; APPLICANT: Wehrman, Tom
; APPLICANT: Ghosh, Malabika
; APPLICANT: Wang, Dunrui
; APPLICANT: Zhao, Qing A.
; APPLICANT: Wang, Zhwei
; TITLE OF INVENTION: No. US20040048249A1el Nucleic Acids and
; FILE OF INVENTION: Secreted Polypeptides
; FILE REFERENCES: 805A
; CURRENT APPLICATION NUMBER: US/10/112,944
; CURRENT FILING DATE: 2002-03-28
; PRIOR APPLICATION NUMBER: US 09/488,725
; PRIOR FILING DATE: 2000-01-21
; PRIOR APPLICATION NUMBER: US 09/431,404
; PRIOR FILING DATE: 2000-01-25
; PRIOR APPLICATION NUMBER: US 09/436,914
; PRIOR FILING DATE: 2000-02-03
; PRIOR APPLICATION NUMBER: US 09/515,126
; PRIOR FILING DATE: 2000-02-28
; PRIOR APPLICATION NUMBER: US 09/519,705
; PRIOR FILING DATE: 2000-03-07
; PRIOR APPLICATION NUMBER: US 09/540,217
; PRIOR FILING DATE: 2000-03-31
; PRIOR APPLICATION NUMBER: US 09/552,929
; PRIOR FILING DATE: 2000-04-18
; PRIOR APPLICATION NUMBER: US 09/577,408
; PRIOR FILING DATE: 2000-05-18

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Db 920 ACAAACACATTTAAGATAAATGATCTGCAAACTCTCTTTTAATGATGAAGAGATGAAA 979
QY 901 AATGTAATGGATTCTTCAAAATGACATTTCTGTAATACCTGGATCTATCTTCCCTCGACCA 960
Db 980 AATGTAATGGATTCTTCAAAATGACATTTCTGTAATACCTGGATCTATCTTCCCTCGACCA 1039
QY 961 GTAGAAATTTTAAACACAGTGCAGAAATCAGTTACAGTATTTCAAGAAATGTAAGCACT 1020
Db 1040 GTAGAAATTTTAAACACAGTGCAGAAATCAGTTACAGTATTTCAAGAAATGTAAGCACT 1099
QY 1021 AATGTCCTTCTCAAGCAACATGATTACATCATTTAGTTTGTGATTTATATCTACTGTCCTG 1080
Db 1100 AATGTCCTTCTCAAGCAACATGATTACATCATTTAGTTTGTGATTTATATCTACTGTCCTG 1159
QY 1081 AAGCCATCTCTCAACCTCAGCCACTGTGAAGTTAACTCGTCTGATGGCAACCAACTG 1140
Db 1160 AAGCCATCTCTCAACCTCAGCCACTGTGAAGTTAACTCGTCTGATGGCAACCAACTG 1219
QY 1141 ACTCTTGAAGAAAGAAAGAAATATGATGATCATTAACAGTGCAGAGAACTATCTGAG 1200
Db 1220 ACTCTTGAAGAAAGAAAGAAATATGATGATCATTAACAGTGCAGAGAACTATCTGAG 1279
QY 1201 TACTGAGCGGATCTAACAGTGGAAATCAGAAATGGAAGCTGTTTCAGAAAAATAAATTAT 1260
Db 1280 TACTGAGCGGATCTAACAGTGGAAATCAGAAATGGAAGCTGTTTCAGAAAAATAAATTAT 1339
QY 1261 ACTGTCCCAAGAGTGGAACTTTAAGATTGANTCCCAATCCGAGGANTCCAGTGAG 1320
Db 1340 ACTGTCCCAAGAGTGGAACTTTAAGATTGANTCCCAATCCGAGGANTCCAGTGAG 1399
QY 1321 CTACAGTTGAAGCCCTATTTCCTTGTGTAGTAAAGTAGCATGCGACGTTCATAGTCTGTTT 1380
Db 1400 CTACAGTTGAAGCCCTATTTCCTTGTGTAGTAAAGTAGCATGCGACGTTCATAGTCTGTTT 1459
QY 1381 AAGTCTCTTAGTAAGACATACATCCAACTNAAACCAAGAGATGAAATATAAGGTGGGA 1440
Db 1460 AAGTCTCTTAGTAAGACATACATCCAACTNAAACCAAGAGATGAAATATAA----- 1512
QY 1441 TCGCCCTTTGAGTTGGTGTAGTGGCAACAAACGATTGAAGAGTTAAGCTATATGTA 1500
Db 1513 -----GGTA 1516
QY 1501 GTATCCAGGGACAGTTGGTGGCTGTAGGAAAAACAAATTCACAAATGTTCTTTAAACA 1560
Db 1517 GTATCCAGGGACAGTTGGTGGCTGTAGGAAAAACAAATTCACAAATGTTCTTTAAACA 1576
QY 1561 CCAGAAATTTCTGGACTCCAAAGCCTGTGTAATTGTGTATTATATTGAGATGATGG 1620
Db 1577 CCAGAAATTTCTGGACTCCAAAGCCTGTGTAATTGTGTATTATATTGAGATGATGG 1636
QY 1621 GAAATATAAGTGAATGTTCTAAAAATTCCTGTTTCAAGCTTGTGTTTAAAAATAGATAAAG 1680
Db 1637 GAAATATAAGTGAATGTTCTAAAAATTCCTGTTTCAAGCTTGTGTTTAAAAATAGATAAAG 1696
QY 1681 CTATATTGGAGTAAAGTGAAGCTGAACCATCTGAGAAAGTCTCTCTTAGGATCTCTGTG 1740
Db 1697 CTATATTGGAGTAAAGTGAAGCTGAACCATCTGAGAAAGTCTCTCTTAGGATCTCTGTG 1756
QY 1741 ACACAGCTGACCTCAGTTGGATTGAGTTGAGCTTGTGACAAAAGTGTGAATCTGATGAAT 1800
Db 1757 ACACAGCTGACCTCAGTTGGATTGAGTTGAGCTTGTGACAAAAGTGTGAATCTGATGAAT 1816
QY 1801 GCCTCTAATGATATTACAATGGAATGTTG 1830
Db 1817 GCCTCTAATGATATTACAATGGAATGTTG 1846

RESULT 4
US-10-264-237-1040
; Sequence 1040, Application US/10264237
; Publication No. US20040009491A1
; GENERAL INFORMATION:
; APPLICANT: Birse et al.

; TITLE OF INVENTION: Nucleic Acids, Proteins, and Antibodies
; FILE REFERENCE: PA131PI
; CURRENT APPLICATION NUMBER: US/10/264,237
; CURRENT FILING DATE: 2002-10-04
; PRIOR APPLICATION NUMBER: PCT/US01/16450
; PRIOR FILING DATE: 2001-05-18
; PRIOR APPLICATION NUMBER: US 60/205,515
; PRIOR FILING DATE: 2000-05-19
; NUMBER OF SEQ ID NOS: 2876
; SOFTWARE: PatentIn ver. 3.1
; SEQ ID NO 1040
; LENGTH: 1448
; TYPE: DNA
; ORGANISM: Homo sapiens
US-10-264-237-1040

Query Match 23.7%; Score 1017; DB 16; Length 1448;
Best Local Similarity 95.5%; Pred. No. 1.6e-255;
Matches 1078; Conservative 0; Mismatches 0; Indels 51; Gaps 1;
QY 3210 GTCATATCCATTTTGGAGTCTGAAATTCAGTAGAGGAATTTTCAGACAATATATCTCTAGC 3269
Db 1 GTCATATCCATTTTGGAGTCTGAAATTCAGTAGAGGAATTTTCAGACAATATATCTCTAGC 60
QY 3270 CTTTATAACTTTATGCAATTTGTCATCAGTGGGGAGTCTTAAAGCGAAGGAAGCTTTTGAATAT 3329
Db 61 CTTTATAACTTTATGCAATTTGTCATCAGTGGGGAGTCTTAAAGCGAAGGAAGCTTTTGAATAT 120
QY 3330 GCTGACTTGGAGAGCAGAACAAAGAGGTGGCATGCAATCTTGGGTGTCATCAGATGCCAA 3389
Db 121 GCTGACTTGGAGAGCAGAACAAAGAGGTGGCATGCAATCTTGGGTGTCATCAGATGCCAA 180
QY 3390 ACTTTCTGACTCTCTGGCAGCCACGCTCCCTGGATATTAAGTTGCGAGCTATGCACTGCT 3449
Db 181 ACTTTCTGACTCTCTGGCAGCCACGCTCCCTGGATATTAAGTTGCGAGCTATGCACTGCT 240
QY 3450 CTCACACTCTTACAAATTTTTCAGACTTTGAGGGGAATCCCAATTTATGAGGTGGCTAAGCAG 3509
Db 241 CTCACACTCTTACAAATTTTTCAGACTTTGAGGGGAATCCCAATTTATGAGGTGGCTAAGCAG 300
QY 3510 GCAAGAAATAGCTTGGGTGGTGGTTCATCTACTCAGATACCACTGTGGCTTTAAAGGC 3569
Db 301 GCAAGAAATAGCTTGGGTGGTGGTTCATCTACTCAGATACCACTGTGGCTTTAAAGGC 360
QY 3570 TCTGTCTGAATTTGAGCCCTTAATGAATACAGAAAGGACAAATATCCAAGTGCAGCTGAC 3629
Db 361 TCTGTCTGAATTTGAGCCCTTAATGAATACAGAAAGGACAAATATCCAAGTGCAGCTGAC 420
QY 3630 GGGGCTAGCTCACCAGTCTCT----- 3651
Db 421 GGGGCTAGCTCACCAGTCTCTCTAAAGTTCTGATTGACACACACACCGCTTACTCCT 480
QY 3652 -----CTTGTGTGGTACAGCCAATGGCAGTTAATATTTCCGCAAAATGGTTT 3698
Db 481 TCAGACAGCAGAGCTTGTGTGTACAGCCAATGGCAGTTAATATTTCCGCAAAATGGTTT 540
QY 3699 TGGATTGCTATTCTCAGCTCAATGTTGTATATATGTAAGGCTTCTGGTCTTCTAG 3758
Db 541 TGGATTGCTATTCTCAGCTCAATGTTGTATATATGTAAGGCTTCTGGTCTTCTAG 600
QY 3759 AAGACGAGATCTATCCAAATTCAGAAAGCTTTGATTTAGATGTTGCTGTAAGAAAAA 3818
Db 601 AAGACGAGATCTATCCAAATTCAGAAAGCTTTGATTTAGATGTTGCTGTAAGAAAAA 660
QY 3819 TAAAGATGATCTCAATCATGTTGAATTTGAATGTTGTAACAAGTTTTTGGGCCCGGGTAG 3878
Db 661 TAAAGATGATCTCAATCATGTTGAATTTGAATGTTGTAACAAGTTTTTGGGCCCGGGTAG 720
QY 3879 GAGTGGCATGGCTTCTTATGGAGTTAACTTATTAAGTGGCTTTATGGCTTCAGAGGC 3938
Db 721 GAGTGGCATGGCTTCTTATGGAGTTAACTTATTAAGTGGCTTTATGGCTTCAGAGGC 780
QY 3939 AATTTCTCTGAGCGAGACAGTGCAGAAAGTGGAAATATGATCATGGAATACTCAACCTCTA 3998

NUMBER OF SEQ ID NOS: 271
; SOFTWARE: PERL Program
; SEQ ID NO 223
; LENGTH: 1300
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: misc feature
; OTHER INFORMATION: Incyte ID No. US20030166903A1 3658034cB1
US-10-133-013-223

Query Match 17.0%; Score 730.8; DB 15; Length 1300;
Best Local Similarity 93.6%; Pred. No. 2e-180;
Matches 805; Conservative 0; Mismatches 2; Indels 53; Gaps 2;

QY 3479 AGGGATCCCAATATAGAGTGGCTAAGCAGCGGAAAGAAATAGCTTGGGTGGTTTGCAT 3538
DB 1 AGGGAATCCCAATATAGAGCGGCTAAGCAGCGGAAAGAAATAGCTTGGGTGGTTTGCAT 60
QY 3539 CTACTCAGGATACACCTGTGGCTTTAAAGGCTCTGTCTGAATTTGAGCGCTTAATGAATA 3598
DB 61 CTACTCAGGATACACCTGTGGCTTTAAAGG--CTGTCTGAATTTGAGCGCTTAATGAATA 118
QY 3599 CAGAAAGGACAAATATCCAAAGTACCGTGACGGGCTAGCTCACCAAGTCCT----- 3651
DB 119 CAGAAAGGACAAATATCCAAAGTACCGTGACGGGCTAGCTCACCAAGTCCTGTAAGT 178
QY 3652 -----CTTGTCTGGTACAGC 3667
DB 179 TTCTGATTTGACACACACACCGCTTACTCTCTCAGACAGCAGCTTGTGGTACAGC 238
QY 3668 CAATGGCAGTTAATATTCGCGAAATGGTTTGGATTGCTATTTGTCAGCTCAATGTTG 3727
DB 239 CAACGGCAGTTAATATTCGCGAAATGGTTTGGATTGCTATTTGTCAGCTCAATGTTG 298
QY 3728 TATATAATGTGAAGCTTCTGGCTCTCTAGAGACGAGATCTATCCAAATCAGAG 3787
DB 299 TATATAATGTGAAGCTTCTGGCTCTCTAGAGACGAGATCTATCCAAATCAGAG 358
QY 3788 CCTTTGATTTAGATTTGCTGTAAGAAATAAAGATGATCTCAATCATGTGGATTGA 3847
DB 359 CCTTTGATTTAGATTTGCTGTAAGAAATAAAGATGATCTCAATCATGTGGATTGA 418
QY 3848 ATGTGTGTA CAAGCTTTTCGGGCCGGGTAGAGTGCATGCTCTTAAGAAAGTTAAAC 3907
DB 419 ATGTGTGTACAAGCTTTTCGGGCCGGGTAGAGTGCATGCTCTTAAGAAAGTTAAAC 478
QY 3908 TATTAAGTGGCTTTATGGTGCCTTCAGAACCAATTTCTGAGCGAGACAGTGAAGAAAG 3967
DB 479 TATTAAGTGGCTTTATGGTGCCTTCAGAACCAATTTCTGAGCGAGACAGTGAAGAAAG 538
QY 3968 TGAATAATGATCATGGAAAACTCAACCTCTATTAGATTCTGTAATGAAACCCAGTTTT 4027
DB 539 TGAATAATGATCATGGAAAACTCAACCTCTATTAGATTCTGTAATGAAACCCAGTTTT 598
QY 4028 GTGTTAATATCTGCTGTGAGAACTTTAAAGTTTCAATATCCAGATGCTTCAGTGT 4087
DB 599 GTGTTAATATCTGCTGTGAGAACTTTAAAGTTTCAATATCCAGATGCTTCAGTGT 658
QY 4088 CCAATAGTGGATTACTATGAGCCAAAGGACAGCGGCTGAGAAGTTACAACCTCTGAAAGTGA 4147
DB 659 CCAATAGTGGATTACTATGAGCCAAAGGACAGCGGCTGAGAAGTTACAACCTCTGAAAGTGA 718
QY 4148 AGCTGTCTCTGTGACCTTTGAGTGAATGTCAGGCTCCCGTCTTGTGAGGATGGAG 4207
DB 719 AGCTGTCTCTGTGACCTTTGAGTGAATGTCAGGCTCCCGTCTTGTGAGGATGGAG 778
QY 4208 CTTTCAGGCTCCCATCATCACTCTCACTCATTTTATTTTCTGTTTCAAGCTTCTGACT 4267
DB 779 CTTTCAGGCTCCCATCATCACTCTCACTCATTTTATTTTCTGTTTCAAGCTTCTGACT 838
QY 4268 TTATGGAACCTTTGGCTGTGA 4287

DB 839 TTATGGAACCTTTGGCTGTGA 858

RESULT 7
US-09-820-649-48
; Sequence 48, Application US/09820649
; Publication No. US20030199683A1
; GENERAL INFORMATION:
; APPLICANT: Ruben et al.
; TITLE OF INVENTION: 83 Human Secreted Proteins
; FILE REFERENCE: PZ012P1
; CURRENT APPLICATION NUMBER: US/09/820,649
; CURRENT FILING DATE: 2001-03-30
; PRIOR APPLICATION NUMBER: US/09/236,557
; PRIOR FILING DATE: 1999-01-26
; PRIOR APPLICATION NUMBER: PCT/US98/15949
; PRIOR FILING DATE: 1998-07-29
; PRIOR APPLICATION NUMBER: 60/054,212
; PRIOR FILING DATE: 1997-07-30
; PRIOR APPLICATION NUMBER: 60/054,209
; PRIOR FILING DATE: 1997-07-30
; PRIOR APPLICATION NUMBER: 60/054,234
; PRIOR FILING DATE: 1997-07-30
; PRIOR APPLICATION NUMBER: 60/054,218
; PRIOR FILING DATE: 1997-07-30
; PRIOR APPLICATION NUMBER: 60/054,214
; PRIOR FILING DATE: 1997-07-30
; PRIOR APPLICATION NUMBER: 60/054,236
; PRIOR FILING DATE: 1997-07-30
; PRIOR APPLICATION NUMBER: 60/054,215
; PRIOR FILING DATE: 1997-07-30
; PRIOR APPLICATION NUMBER: 60/054,211
; PRIOR FILING DATE: 1997-07-30
; Remaining Prior Application data removed - See File Wrapper or PALM.
; NUMBER OF SEQ ID NOS: 353
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 48
; LENGTH: 875
; TYPE: DNA
; ORGANISM: Homo sapiens
US-09-820-649-48

Query Match 12.6%; Score 541.6; DB 10; Length 875;
Best Local Similarity 99.8%; Pred. No. 6.8e-131;
Matches 541; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 3746 CTGGTCTTCTAGAGACGAAAGATCTATCCAAAATCAAGAGCCCTTTCATTAGATGTG 3805
DB 15 CTGGTCTTCTAGAGACGAAAGATCTATCCAAAATCAAGAGCCCTTTCATTAGATGTG 74
QY 3806 CTGTAAGAGAAATTAAGATGATCTCAATCATGTGGATTGAATGTGTACAAAGCTTTT 3865
DB 75 CTGTAAGAGAAATTAAGATGATCTCAATCATGTGGATTGAATGTGTACAAAGCTTTT 134
QY 3866 CGGGCCCGGTAGGAGTGGCATGGCTCTTATGGAAGTTAACTATTAAAGTGGCTTTATGG 3925
DB 135 CGGGCCCGGTAGGAGTGGCATGGCTCTTATGGAAGTTAACTATTAAAGTGGCTTTATGG 194
QY 3926 TGCCTTCAGAGCAATTTCTCTGAGCGAGACAGTGAAGAAAGTGAATATGATCATGAA 3985
DB 195 TGCCTTCAGAGCAATTTCTCTGAGCGAGACAGTGAAGAAAGTGAATATGATCATGAA 254
QY 3986 AACTCAACCTCTATTAGATTTCTGTAATGAAACCCAGTTTGTGTTAATATTCCTGCTG 4045
DB 255 AACTCAACCTCTATTAGATTTCTGTAATGAAACCCAGTTTGTGTTAATATTCCTGCTG 314
QY 4046 TGAGAAACTTTTAAAGTTTCAATATCCCAAGATGCTTCAGTGTCCATAGTGGATTACTATG 4105
DB 315 TGAGAAACTTTTAAAGTTTCAATATCCCAAGATGCTTCAGTGTCCATAGTGGATTACTATG 374
QY 4106 AGCCAAGAGACAGCGCGGTGAGAGTTACAACCTCTGAAGTGAAGCTGCTCCTCTGAC 4165
DB 375 AGCCAAGAGACAGCGCGGTGAGAGTTACAACCTCTGAAGTGAAGCTGCTCCTCTGAC 434

4166	TTTCAGTGATGTCACAGGCTCGGCTCTTGTCAGATCGAGCTTCAGCTCCCATCATC	4325
Qy		
435	TTTCAGTGATGTCACAGGCTCGGCTCTTGTCAGATCGAGCTTCAGCTCCCATCATC	494
Db		
4226	ACTCTTCAGTCATTTTATTTTCTGTTTCAAGCTTCGTACTCTTATGGAACCTTTGGCTGT	4385
Qy		
495	AMTCTTCAGTCATTTTATTTTCTGTTTCAAGCTTCGTACTCTTATGGAACCTTTGGCTGT	554
Db		
4286	GA 4287	
Qy		
555	GA 556	
Db		

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RESULT 8
US-10-160-162-48
/ Sequence 48, Application US/10160162
/ Publication No. US20030166541a1
/ GENERAL INFORMATION:
/ APPLICANT: Ruben et al.
/ TITLE OF INVENTION: 83 Human Secreted Proteins
/ FILE REFERENCE: PZ01252
/ CURRENT APPLICATION NUMBER: US/10/160,162
/ CURRENT FILING DATE: 2002-06-04
/ PRIOR APPLICATION NUMBER: 60/295,558
/ PRIOR FILING DATE: 2001-06-05
/ PRIOR APPLICATION NUMBER: 09/236,557
/ PRIOR FILING DATE: 1999-01-26
/ PRIOR APPLICATION NUMBER: PCT/US98/15949
/ PRIOR FILING DATE: 1998-07-29
/ PRIOR APPLICATION NUMBER: 60/054,212
/ PRIOR FILING DATE: 1997-07-30
/ PRIOR APPLICATION NUMBER: 60/054,209
/ PRIOR FILING DATE: 1997-07-30
/ PRIOR APPLICATION NUMBER: 60/054,234
/ PRIOR FILING DATE: 1997-07-30
/ PRIOR APPLICATION NUMBER: 60/054,218
/ PRIOR FILING DATE: 1997-07-30
/ PRIOR APPLICATION NUMBER: 60/054,214
/ PRIOR FILING DATE: 1997-07-30
/ PRIOR APPLICATION NUMBER: 60/054,236
/ PRIOR FILING DATE: 1997-07-30
/ PRIOR APPLICATION NUMBER: 60/054,215
/ PRIOR FILING DATE: 1997-07-30
/ PRIOR APPLICATION NUMBER: 60/054,211
/ PRIOR FILING DATE: 1997-07-30
/ PRIOR APPLICATION NUMBER: 60/054,217
/ PRIOR FILING DATE: 1997-07-30
/ PRIOR APPLICATION NUMBER: 60/054,213
/ PRIOR FILING DATE: 1997-07-30
/ PRIOR APPLICATION NUMBER: 60/055,968
/ PRIOR FILING DATE: 1997-08-18
/ PRIOR APPLICATION NUMBER: 60/055,969
/ PRIOR FILING DATE: 1997-08-18
/ PRIOR APPLICATION NUMBER: 60/055,972
/ PRIOR FILING DATE: 1997-08-18
/ PRIOR APPLICATION NUMBER: 60/056,561
/ PRIOR FILING DATE: 1997-08-19
/ PRIOR APPLICATION NUMBER: 60/056,534
/ PRIOR FILING DATE: 1997-08-19
/ PRIOR APPLICATION NUMBER: 60/056,729
/ PRIOR FILING DATE: 1997-08-19
/ PRIOR APPLICATION NUMBER: 60/056,543
/ PRIOR FILING DATE: 1997-08-19
/ PRIOR APPLICATION NUMBER: 60/056,727
/ PRIOR FILING DATE: 1997-08-19
/ PRIOR APPLICATION NUMBER: 60/056,554
/ PRIOR FILING DATE: 1997-08-19
/ PRIOR APPLICATION NUMBER: 60/056,730
/ PRIOR FILING DATE: 1997-08-19
/ NUMBER OF SEQ ID NOS: 353
/ SOFTWARE: PatentIn Ver. 2.0
/ SEQ ID NO 48

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; LENGTH: 875
; TYPE: DNA
; ORGANISM: Homo sapiens
US-10-160-162-48

Query Match 12.6%; Score 541.6; DB 15; Length 875;
Best Local Similarity 99.8%; Pred. No. 6.8e-131;
Matches 541; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 3746 CTGGGCTCTTCTAGAACGACGAAGATCTATCCAAATCAAGAAAGCCTTTGATTTAGATGTTG 3805
Db 15 CTGGGCTCTTCTAGAACGACGAAGATCTATCCAAATCAAGAAAGCCTTTGATTTAGATGTTG 74
QY 3806 CTGTAAAGAAATAAAGATGATCTCAATCATGTGGATTTGAATGTGTACAAAGCTTTT 3865
Db 75 CTGTAAAGAAATAAAGATGATCTCAATCATGTGGATTTGAATGTGTACAAAGCTTTT 134
QY 3866 CGGGCCCGGGTAGGAGTGGCATGGCTCTTATGGAAGTTAACTTATTAAGTGGCTTTATGG 3925
Db 135 CGGGCCCGGGTAGGAGTGGCATGGCTCTTATGGAAGTTAACTTATTAAGTGGCTTTATGG 194
QY 3926 TGGCTTCAGAAGCAATTTCTCTGAGCGACACAGTGAAGAAAGTGGAAATATGATCATCGAA 3985
Db 195 TGGCTTCAGAAGCAATTTCTCTGAGCGACACAGTGAAGAAAGTGGAAATATGATCATCGAA 254
QY 3986 AACTCAACCTCTATTTAGATTTCTGTAATTAACACCCAGTTTTGTGTATAATTCTCTGCTG 4045
Db 255 AACTCAACCTCTATTTAGATTTCTGTAATTAACACCCAGTTTTGTGTATAATTCTCTGCTG 314
QY 4046 TGAGAAACCTTTAAAGTTTCAATATACCAAGATGCTTTCAGTGCCATAGTGGATTACTATG 4105
Db 315 TGAGAAACCTTTAAAGTTTCAATATACCAAGATGCTTTCAGTGCCATAGTGGATTACTATG 374
QY 4106 AGCCRAGGACAGCGGGTGAGAGTTTACAACTCTGAAGTGAAGCTGTCTCTCTGTGACC 4165
Db 375 AGCCRAGGACAGCGGGTGAGAGTTTACAACTCTGAAGTGAAGCTGTCTCTCTGTGACC 434
QY 4166 TTTGCAGTGATGTCCAGGCTGCCGTCCTTGTGAGGATCGAAGCTTCAGGCTCCCATCATC 4225
Db 435 TTTGCAGTGATGTCCAGGCTGCCGTCCTTGTGAGGATCGAAGCTTCAGGCTCCCATCATC 494
QY 4226 ACTCTTCAGTCATTTTATTTCTGTCTTCAAGCTTCTGACTTTATGGAACCTTGGCTGT 4285
Db 495 AMTCTTCAGTCATTTTATTTCTGTCTTCAAGCTTCTGACTTTATGGAACCTTGGCTGT 554
QY 4286 GA 4287
Db 555 GA 556

RESULT 9
US-10-211-462-208
; Sequence 208, Application US/10211462
; Publication No. US20040033495A1
; GENERAL INFORMATION:
; APPLICANT: Murray, Richard
; APPLICANT: Glynn, Richard
; APPLICANT: Watson, Susan R.
; APPLICANT: Aziz, Natsaha
; APPLICANT: Eos Biotechnology, Inc.
; TITLE OF INVENTION: Methods of Diagnosis of Angiogenesis, Compositions and
; TITLE OF INVENTION: Methods of Screening for Angiogenesis Modulators
; FILE REFERENCE: 018501-008200US
; CURRENT APPLICATION NUMBER: US/10/211,462
; CURRENT FILING DATE: 2003-02-13
; PRIOR APPLICATION NUMBER: US 09/784,356
; PRIOR FILING DATE: 2001-02-14
; PRIOR APPLICATION NUMBER: US 09/791,390
; PRIOR FILING DATE: 2001-02-22
; PRIOR APPLICATION NUMBER: US 60/310,025
; PRIOR FILING DATE: 2001-08-03
; PRIOR APPLICATION NUMBER: US 60/334,244
; PRIOR FILING DATE: 2001-11-29

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; NUMBER OF SEQ ID NOS: 230
; SOFTWARE: Patentin Ver. 2.1
; SEQ ID NO 208
; LENGTH: 821
; TYPE: DNA
; ORGANISM: Homo sapiens
US-10-211-462-208

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Query Match	12.23;	Score 525;	DB 13;	Length 821;
Best Local Similarity	100.0%;	Prod. No. 1.5e-126;		
Matches 525;	Conservative 0;	Mismatches 10;	Gaps 0;	
QY	3763	CGAAGATCTATCCAAAATCAAGAAAGCCCTTTGATTTAGATGTGCTGTAAAGAAAAATAAA	3822	
Db	1	CGAAGATCTATCCAAAATCAAGAAAGCCCTTTGATTTAGATGTGCTGTAAAGAAAAATAAA	60	
QY	3823	GATGATCTCAATCATGTGGATTTGAATGTGTGTACAAAGCTTTTCGGGCCCGGGTAGGAGT	3882	
Db	61	GATGATCTCAATCATGTGGATTTGAATGTGTGTACAAAGCTTTTCGGGCCCGGGTAGGAGT	120	
QY	3883	GGCATGGCTCTTATGGAAGTTAACTATTAAAGTGGCTTTATGGTGGCCCTCAGAAGCAATT	3942	
Db	121	GGCATGGCTCTTATGGAAGTTAACTATTAAAGTGGCTTTATGGTGGCCCTCAGAAGCAATT	180	
QY	3943	TCTCTGAGCGAGACAGTGAAGAAAGTGGAAATATGATCATGAAAACTCAACCTCTATTTA	4002	
Db	181	TCTCTGAGCGAGACAGTGAAGAAAGTGGAAATATGATCATGAAAACTCAACCTCTATTTA	240	
QY	4003	GATTCTCTGTAATGAAACCCAGTTTGTGTAAATATTCCTGCTGTGAGAAACTTTTAAAGTT	4062	
Db	241	GATTCTCTGTAATGAAACCCAGTTTGTGTAAATATTCCTGCTGTGAGAAACTTTTAAAGTT	300	
QY	4063	TCAAATACCCAAAGATGCTTCAGTGTCCANAGTGGATTACTATAGGCCAAGGAGACAGCG	4122	
Db	301	TCAAATACCCAAAGATGCTTCAGTGTCCATAGTGGATTACTATAGGCCAAGGAGACAGCG	360	
QY	4123	GTGAGAGATTACAACCTCTGAAGTCAAGCTGTCCTCTGTGACCTTTGCAGTGATGTCAG	4182	
Db	361	GTGAGAGATTACAACCTCTGAAGTCAAGCTGTCCTCTGTGACCTTTGCAGTGATGTCAG	420	
QY	4183	GGCTGGCGTCTCTGTGAGGATGGAGCTTCAGGCTCCCATCATCACTCTTCAGTCATTTTT	4242	
Db	421	GGCTGGCGTCTCTGTGAGGATGGAGCTTCAGGCTCCCATCATCACTCTTCAGTCATTTTT	480	
QY	4243	ATTTCCTGTTTCAAGCTTCTGTACTTTATGGAACCTTTGGCTGTGA	4287	
Db	481	ATTTCCTGTTTCAAGCTTCTGTACTTTATGGAACCTTTGGCTGTGA	525	

RESULT 10
US-10-085-783A-45412
; Sequence 45412, Application US/10085783A
; Publication No. US20040037841A1
; GENERAL INFORMATION:
; APPLICANT: ChondroGene Inc.
; APPLICANT: Liew, C.C.
; TITLE OF INVENTION: Compositions and Methods Relating to Osteoarthritis
; FILE REFERENCE: 4231/2002
; CURRENT APPLICATION NUMBER: US/10/085,783A
; CURRENT FILING DATE: 2002-02-28
; CURRENT APPLICATION NUMBER: US 60/305,340
; PRIOR FILING DATE: 2001-07-13
; PRIOR APPLICATION NUMBER: US 60/275,017
; PRIOR FILING DATE: 2001-03-12
; PRIOR APPLICATION NUMBER: US 60/271,955
; PRIOR FILING DATE: 2001-02-28
; NUMBER OF SEQ ID NOS: 58994
; SOFTWARE: Patent in version 3.2
; SEQ ID NO 45412
; LENGTH: 520
; TYPE: DNA
; ORGANISM: Human
US-10-085-783A-45412

Query Match	11.6%;	Score	497.4;	DB	13;	Length	520;
Best Local Similarity	99.8%;	Pred. No.	1.8e-119;				
Matches	509;	Conservative	0;	Mismatches	1;	Indels	1;
Gaps	1;						
Qy	2872	AGGCAAGGTTACCA-CAGAGAACTTCTCTATCAGAGGGAAGATGGGCTCTTTCAGTGCCTTT	2930				
Db	1	AGGCAAGGTTACCATGAGAGAACTTCTCTATCAGAGGGAAGATGGGCTCTTTCAGTGCCTTT	60				
Qy	2931	TGGGAATTATGACCCCTTCTGGGAGCACTTGTTGTGTCAGCTTTGTGTTTAAAGATGTTTCCT	2990				
Db	61	TGGGAATTATGACCCCTTCTGGGAGCACTTGTTGTGTCAGCTTTGTGTTTAAAGATGTTTCCT	120				
Qy	2991	TGAAGCGGATCCTTACATAGATATTGATCAGATGTGTTTACAGAGAACATACACTTCGGCT	3050				
Db	121	TGAAGCGGATCCTTACATAGATATTGATCAGATGTGTTTACAGAGAACATACACTTCGGCT	180				
Qy	3051	TAAAGGACATCAAAATCCAAACGGTGAATTTTGGGATCCAGGAAGAGTGATTCATAGTGA	3110				
Db	181	TAAAGGACATCAAAATCCAAACGGTGAATTTTGGGATCCAGGAAGAGTGATTCATAGTGA	240				
Qy	3111	GCTTCAAGGTGGCAATAAAAGTCCAGTAAACATTTACAGCCTATATTGTATACTCTCTCCT	3170				
Db	241	GC'TTCAAGGTGGCAATAAAAGTCCAGTAAACATTTACAGCCTATATTGTATACTCTCTCCT	300				
Qy	3171	GGGATATAGAAAGTATCAGGCTAACATTTGATGTGCAAGAGTCTATCCATTTTGGAGTC	3230				
Db	301	GGGATATAGAAAGTATCAGGCTAACATTTGATGTGCAAGAGTCTATCCATTTTGGAGTC	360				
Qy	3231	TGAATTCAGTATAGAGGAATTTTCAGACAAATTAATCTCTAGCCCTTATTAACCTTATGCAATGTC	3290				
Db	361	TGAATTCAGTATAGAGGAATTTTCAGACAAATTAATCTCTAGCCCTTATTAACCTTATGCAATGTC	420				
Qy	3291	ATCAGTGGGAGTCCCTAAAGCGAAGGAAGCTTTGAAATATCTGACTTGGAGAGCAGAACA	3350				
Db	421	ATCAGTGGGAGTCCCTAAAGCGAAGGAAGCTTTGAAATATCTGACTTGGAGAGCAGAACA	480				
Qy	3351	AGAAGTGGCATGCAATCTTGGGTGTCATCA	3381				
Db	481	AGAAGTGGCATGCAATCTTGGGTGTCATCA	511				

RESULT 11

US-10-242-535A-45412

Sequence 45412, Application US/10242535A

Publication No. US20040013663A1

GENERAL INFORMATION:

APPLICANT: ChondroGene Inc.

APPLICANT: Liew, C.C.

TITLE OF INVENTION: Compositions and Methods Relating to Osteoarthritis

FILE REFERENCE: 4231/2005

CURRENT APPLICATION NUMBER: US/10/242,535A

CURRENT FILING DATE: 2002-09-12

PRIOR APPLICATION NUMBER: US 10/085,783

PRIOR FILING DATE: 2002-02-28

PRIOR APPLICATION NUMBER: US 60/305,340

PRIOR FILING DATE: 2001-07-13

PRIOR APPLICATION NUMBER: US 60/275,017

PRIOR FILING DATE: 2001-03-12

PRIOR APPLICATION NUMBER: US 60/271,955

PRIOR FILING DATE: 2001-02-28

NUMBER OF SEQ ID NOS: 58994

SOFTWARE: PatentIn version 3.2

SEQ ID NO 45412

LENGTH: 520

TYPE: DNA

ORGANISM: Human

US-10-242-535A-45412

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Query Match      11.6%; Score 497.4; DB 16; Length 520;
Best Local Similarity 99.6%; Pred. No. 1.8e-119;
Matches 509; Conservative 0; Mismatches 1; Indels 1; Gaps 1;
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2872	QY	AGCAAGGTTACCA-GAGAGAACTTCTCTATCAGAGGAGATGGCTCTTTTCAGTGCCTT	2930
1	Db	AGGCAAGGTTACCATGAGAGAACTTCTCTATCAGAGGGAAGATGGCTCTTTTCAGTGCCTT	60
2931	QY	TGGGAATTATGACCCCTTCTGGGAGCACTTGGTTGTGTCAGCTTTTGTGTTTAAAGATGTTTCCT	2990
61	Db	TGGGAATTATGACCCCTTCTGGGAGCACTTGGTTGTGTCAGCTTTTGTGTTTAAAGATGTTTCCT	120
2991	QY	TGAAGCGGATCCTTACATAGATATTGATCAGAATGTGTTACACAGAACATACACTTGGCT	3050
121	Db	TGAAGCGGATCCTTACATAGATATTGATCAGAATGTGTTACACAGAACATACACTTGGCT	180
3051	QY	TAAAGGACATCAGAAATCCAAACGGTGAATTTTGGGATCCAGGAAGAGTGATTCATAGTGA	3110
181	Db	TAAAGGACATCAGAAATCCAAACGGTGAATTTTGGGATCCAGGAAGAGTGATTCATAGTGA	240
3111	QY	GCCTCAAGTGGGCAATAAAGTCAGTAAACACTTACAGCCTATATTGTAACTCTCTCCT	3170
241	Db	GCCTCAAGTGGGCAATAAAGTCAGTAAACACTTACAGCCTATATTGTAACTCTCTCCT	300
3171	QY	GGGATATAGAAAGTATCAGGCTTAACATTTGATGTGCAAGAGTCTATCCATTTTGGAGTC	3230
301	Db	GGGATATAGAAAGTATCAGGCTTAACATTTGATGTGCAAGAGTCTATCCATTTTGGAGTC	360
3231	QY	TGAATTCAGTAGAGGAATTTTCAGACAAATATATCTTAGCCCTTATTAACCTTATCGATTGTC	3290
361	Db	TGAATTCAGTAGAGGAATTTTCAGACAAATATATCTTAGCCCTTATTAACCTTATCGATTGTC	420
3291	QY	ATCAGTGGGAGTCTTAAAGCGAAGAGGCTTTGAAATATGCTGACTTTGGAGACGAGAACA	3350
421	Db	ATCAGTGGGAGTCTTAAAGCGAAGAGGCTTTGAAATATGCTGACTTTGGAGACGAGAACA	480
3351	QY	AGAAGTGGCATGCAATTTCTGGGTGTCATCA	3381
481	Db	AGAAGTGGCATGCAATTTCTGGGTGTCATCA	511

RESULT 12

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US-10-085-783A-29628
/ Sequence 29628, Application US/10085783A
/ Publication NO. US20040037841A1
/ GENERAL INFORMATION:
/ APPLICANT: ChondroGene Inc.
/ APPLICANT: Liew, C.C.
/ TITLE OF INVENTION: Compositions and Methods Relating to Osteoarthritis
/ FILE REFERENCE: 4231/2002
/ CURRENT APPLICATION NUMBER: US/10/085,783A
/ CURRENT FILING DATE: 2002-02-28
/ PRIOR APPLICATION NUMBER: US 60/305,340
/ PRIOR FILING DATE: 2001-07-13
/ PRIOR APPLICATION NUMBER: US 60/275,017
/ PRIOR FILING-DATE: 2001-03-12
/ PRIOR APPLICATION NUMBER: US 60/271,955
/ PRIOR FILING DATE: 2001-02-28
/ NUMBER OF SEQ ID NOS: 58994
/ SOFTWARE: PatentIn version 3.2
/ SEQ ID NO 29628
/ LENGTH: 499
/ TYPE: DNA
/ ORGANISM: Human
/ FEATURE:
/ NAME/KEY: misc_feature
/ LOCATION: (5)..(5)
/ OTHER INFORMATION: n is a, c, g, or t
/ FEATURE:
/ NAME/KEY: misc_feature
/ LOCATION: (14)..(14)
/ OTHER INFORMATION: n is a, c, g, or t
/ FEATURE:
/ NAME/KEY: misc_feature
/ LOCATION: (41)..(41)
/ OTHER INFORMATION: n is a, c, g, or t
/ FEATURE:

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QY 3760 AGACGAAGATCTATCCAAATCAAGAGCCTTTGATTAGATGTTCTGTAAAAGA 3815
Db 444 AGACGAAGATCTATCCAAATCAAGAGCCTTTGATTAGATGTTCTGTAAAAGA 499

RESULT 13
US-10-242-535A-29628
; Sequence 29628, Application US/10242535A
; Publication No. US20040013663A1
; GENERAL INFORMATION:
; APPLICANT: ChondroGene Inc.
; APPLICANT: Liew, C.C.
; TITLE OF INVENTION: Compositions and Methods Relating to Osteoarthritis
; FILE REFERENCE: 4231/2005
; CURRENT APPLICATION NUMBER: US/10/242,535A
; CURRENT FILING DATE: 2002-09-12
; PRIOR APPLICATION NUMBER: US 10/085,783
; PRIOR FILING DATE: 2002-02-28
; PRIOR APPLICATION NUMBER: US 60/305,340
; PRIOR FILING DATE: 2001-07-13
; PRIOR APPLICATION NUMBER: US 60/275,017
; PRIOR FILING DATE: 2001-03-12
; PRIOR APPLICATION NUMBER: US 60/271,955
; PRIOR FILING DATE: 2001-02-28
; NUMBER OF SEQ ID NOS: 58994
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 29628
; LENGTH: 499
; TYPE: DNA
; ORGANISM: Human
; FEATURE:
; NAME/KEY: misc_feature
; LOCATION: (5)..(5)
; OTHER INFORMATION: n is a, c, g, or t
; FEATURE:
; NAME/KEY: misc_feature
; LOCATION: (1)..(14)
; OTHER INFORMATION: n is a, c, g, or t
; FEATURE:
; NAME/KEY: misc_feature
; LOCATION: (41)..(41)
; OTHER INFORMATION: n is a, c, g, or t
; FEATURE:
; NAME/KEY: misc_feature
; LOCATION: (50)..(50)
; OTHER INFORMATION: n is a, c, g, or t
; FEATURE:
; NAME/KEY: misc_feature
; LOCATION: (59)..(59)
; OTHER INFORMATION: n is a, c, g, or t
; FEATURE:
; NAME/KEY: misc_feature
; LOCATION: (92)..(92)
; OTHER INFORMATION: n is a, c, g, or t
; FEATURE:
; NAME/KEY: misc_feature
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; FEATURE:
; NAME/KEY: misc_feature
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; FEATURE:
; NAME/KEY: misc_feature
; LOCATION: (182)..(182)
; OTHER INFORMATION: n is a, c, g, or t
; FEATURE:
; NAME/KEY: misc_feature
; LOCATION: (190)..(190)
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; OTHER INFORMATION: n is a, c, g, or t
; FEATURE:
; NAME/KEY: misc_feature
; LOCATION: (287)..(287)
; OTHER INFORMATION: n is a, c, g, or t
; FEATURE:
; NAME/KEY: misc_feature
; LOCATION: (412)..(412)
; OTHER INFORMATION: n is a, c, g, or t
US-10-242-535A-29628

Query Match 7.8%; Score 334.8; DB 16; Length 499;
Best Local Similarity 84.7%; Pred. No. 8.6e-77;
Matches 403; Conservative 0; Mismatches 22; Indels 51; Gaps 1;

QY 3391 CTTTCTGACTCCTGGCAGCCAGCGCTCCCTGCATATTGAAGTTGCAGCTATGCACTGCTC 3450
Db 24 CTTCTTAATACAGAGCAGCCAGCTCCTGATATGAAGCTATGCACTGCTC 83
QY 3451 TCACACTTCTTACAAATTCAGACTTCTGAGGGAATCCCAATTATGAGTGGCTAAGCAGG 3510
Db 84 TCACACTTNTTACAATNTCAGACTTCTGAGGGAATCCCNATTATGANGTGGCTAAGCAGG 143
QY 3511 CAAGAAATAGCTTGGGTGGTGGTTCATCTACTCAGGATACCACTTGGCTTTAAAGGCT 3570
Db 144 CAAGAAATAGCTGGGTGGTGGTTCATCTACTCAGGATACCACTTGGCTTTAAAGGCT 203
QY 3571 CTGTCTGAATTTGCAGCCCTAATGAATACAGAAAGGACAAATATCCCAAGTACCGTGCAG 3630
Db 204 CTGTCTGAATTTGCAGCCCTAATGAATACAGAAAGGACAAATATCCCAAGTACCGTGCAG 263
QY 3631 GGGCTAGCTCACCAGTCCT----- 3651
Db 264 GGGCTAGCTCACCAGTCCTGTNAAGTTTCTGATTGACACACACACCGCTTACTCCTT 323
QY 3652 -----CTTGTCTGTGTACAGCCATGCGCATTTATATTTCCGCAATGGTTT 3699
Db 324 CAGACAGCAGAGCTGTGTGTACAGCCAAATGCGATTAATATTCGCGCAATGGTTT 383
QY 3700 GGATTGTCTATTGTGTCAGCTCAATGTTGTATATATATGTAAGGCTTCTGGTCTTCTAGA 3759
Db 384 GGATTGTCTATTGTGTCAGCTCAATGTTGTATATATATGTAAGGCTTCTGGTCTTCTAGA 443
QY 3760 AGACGAAGATCTATCCAAATCAAGAGCCTTTGATTAGATGTTCTGTAAAAGA 3815
Db 444 AGACGAAGATCTATCCAAATCAAGAGCCTTTGATTAGATGTTCTGTAAAAGA 499

RESULT 14
US-10-085-783A-46128
; Sequence 46128, Application US/10085783A
; Publication No. US20040037841A1
; GENERAL INFORMATION:
; APPLICANT: ChondroGene Inc.
; APPLICANT: Liew, C.C.
; TITLE OF INVENTION: Compositions and Methods Relating to Osteoarthritis
; FILE REFERENCE: 4231/2002
; CURRENT APPLICATION NUMBER: US/10/085,783A
; CURRENT FILING DATE: 2002-02-28
; PRIOR APPLICATION NUMBER: US 60/305,340
; PRIOR FILING DATE: 2001-07-13
; PRIOR APPLICATION NUMBER: US 60/275,017
; PRIOR FILING DATE: 2001-03-12
; PRIOR APPLICATION NUMBER: US 60/271,955
; PRIOR FILING DATE: 2001-02-28
; NUMBER OF SEQ ID NOS: 58994
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 46128
; LENGTH: 303
; TYPE: DNA
; ORGANISM: Human
; FEATURE:
; NAME/KEY: misc_feature
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; LOCATION: (49)..(49)
; OTHER INFORMATION: n is a, c, g, or t
US-10-085-783A-46128

Query Match
Best Local Similarity 98.7%; Score 297.2; DB 13; Length 303;
Matches 299; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

QY 521 ATTGTATCCCAACAGTGGTGTGTCACAAAGAGTCATCTTGGAGTCATTTCCAAAACCTTTTC 580
Db 1 ATTGTATCCCAACAGTGGTGTGTCACAAAGAGTCATCTTGGAGTCATTTCCAAAACCTTTTC 60
QY 581 AGCTATCTTCCCATCCCAATCTTGGTGAAGTGGTCTATTTCAAGTTCAAGTGAATGACCAGA 640
Db 61 AGCTATCTTCCCATCCCAATCTTGGTGAAGTGGTCTATTTCAAGTTCAAGTGAATGACCAGA 120
QY 641 CATATTATCAATCAATTTTCAGTTTTCAGAAATATGTAATACCAAAATTTGAAGTGACTTTGC 700
Db 121 CATATTATCAATCAATTTTCAGTTTTCAGAAATATGTAATACCAAAATTTGAAGTGACTTTGC 180
QY 701 AGACACCAATTTATTTCTATGAATTTCTAAGCAATTTAAATGGTACCATCACGGCAAAGT 760
Db 181 AGACACCAATTTATTTCTATGAATTTCTAAGCAATTTAAATGGTACCATCACGGCAAAGT 240
QY 761 ATACATATGGGAAGCCAGTGAAGAGGAGCGTAACGCTTACATTTTACCTTTATCCCTTTT 820
Db 241 ATACATATGGGAAGCCAGTGAAGAGGAGCGTAACGCTTACATTTTACCTTTATCCCTTTT 300
QY 821 GGG 823
Db 301 GGG 303

RESULT 15

US-10-242-535A-46128
; Sequence 46128, Application US/10242535A
; Publication No. US20040013663A1
; GENERAL INFORMATION:
; APPLICANT: ChondroGene Inc.
; APPLICANT: Liew, C.C.
; TITLE OF INVENTION: Compositions and Methods Relating to Osteoarthritis
; FILE REFERENCE: 4231/2005
; CURRENT APPLICATION NUMBER: US/10/242,535A
; CURRENT FILING DATE: 2002-09-12
; PRIOR APPLICATION NUMBER: US 10/085,783
; PRIOR FILING DATE: 2002-02-28
; PRIOR APPLICATION NUMBER: US 60/305,340
; PRIOR FILING DATE: 2001-07-13
; PRIOR APPLICATION NUMBER: US 60/275,017
; PRIOR FILING DATE: 2001-03-12
; PRIOR APPLICATION NUMBER: US 60/271,955
; PRIOR FILING DATE: 2001-02-28
; NUMBER OF SEQ ID NOS: 58994
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 46128
; LENGTH: 303
; TYPE: DNA
; ORGANISM: Human
; FEATURE:
; NAME/KEY: misc_feature
; LOCATION: (49)..(49)
; OTHER INFORMATION: n is a, c, g, or t
US-10-242-535A-46128

Query Match
Best Local Similarity 98.7%; Score 297.2; DB 16; Length 303;
Matches 299; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

QY 521 ATTGTATCCCAACAGTGGTGTGTCACAAAGAGTCATCTTGGAGTCATTTCCAAAACCTTTTC 580
Db 1 ATTGTATCCCAACAGTGGTGTGTCACAAAGAGTCATCTTGGAGTCATTTCCAAAACCTTTTC 60
QY 581 AGCTATCTTCCCATCCCAATCTTGGTGAAGTGGTCTATTTCAAGTTCAAGTGAATGACCAGA 640

Db 61 AGCTATCTTCCCATCCCAATCTTGGAGACTGGTCTATTTCAAGTTCAAGTGAATGACCAGA 120
QY 641 CATATTATCAATCAATTTTCAGTTTTCAGAAATATGTAATACCAAAATTTGAAGTGACTTTGC 700
Db 121 CATATTATCAATCAATTTTCAGTTTTCAGAAATATGTAATACCAAAATTTGAAGTGACTTTGC 180
QY 701 AGACACCAATTTATTTCTATGAATTTCTAAGCAATTTAAATGGTACCATCACGGCAAAGT 760
Db 181 AGACACCAATTTATTTCTATGAATTTCTAAGCAATTTAAATGGTACCATCACGGCAAAGT 240
QY 761 ATACATATGGGAAGCCAGTGAAGAGGAGCGTAACGCTTACATTTTACCTTTATCCCTTTT 820
Db 241 ATACATATGGGAAGCCAGTGAAGAGGAGCGTAACGCTTACATTTTACCTTTATCCCTTTT 300
QY 821 GGG 823
Db 301 GGG 303

Search completed: August 18, 2004, 05:25:37
Job time : 2200 secs

GenCore version 5.1.6
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OM nucleic - nucleic search, using sw model

Run on: August 17, 2004, 23:19:30 ; Search time 277 Seconds
(without alignments)

Title: US-10-020-095-3
 Perfect score: 4287
 Sequence: 1 atgcaggagccacagctct.....tatggaaactttggctgtga 4287

Scoring table: IDENTITY_NUC
Gapop 10.0 , Gapext 1.0

Searched: 682709 seqs, 277475446 residues

Total number of hits satisfying chosen parameters: 1365418

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Minimum DB seq length: 0
Maximum DB seq length: 2000000000
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Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

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2: /cgn2_6/ptodata/2/ina/5B COMB.seq:**
3: /cgn2_6/ptodata/2/ina/6A COMB.seq:**
4: /cgn2_6/ptodata/2/ina/6B COMB.seq:**
5: /cgn2_6/ptodata/2/ina/PTUTS COMB.seq:**
6: /cgn2_6/ptodata/2/ina/backfillseq1

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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query		DB	ID	Description	
		Match	Length				
1	2584.6	60.3	3033	4	US-09-833-381-1810	Sequence 1810, Ap	
2	110	21.6	4079	4	US-09-016-431-1174	Sequence 1174, Ap	
3	110	21.6	4577	4	US-09-241-606-1	Sequence 1, Appli	
4	108.4	21.5	4792	4	US-09-566-921-109	Sequence 109, App	
5	49	1.1	832	4	US-09-621-976-2813	Sequence 2813, Ap	
C	6	47.4	1.1	7218	1	US-08-232-463-14	Sequence 14, Appli
	7	47.2	1.1	339	4	US-09-311-352B-1	Sequence 1, Appli
8	46.4	1.1	5211	1	US-08-447-411-1	Sequence 1, Appli	
9	45.4	1.1	2802	4	US-09-976-594-924	Sequence 924, App	
10	44	1.1	333	4	US-09-241-606-5	Sequence 5, Appli	
11	44	1.0	750	4	US-09-241-606-3	Sequence 3, Appli	
C	12	42.8	1.0	832	4	US-09-621-976-2813	Sequence 2813, Ap
	13	41.6	1.0	10467	4	US-10-204-708-2	Sequence 2, Appli
14	41.4	1.0	5398	3	US-09-356-952-11	Sequence 11, Appli	
C	15	41.4	1.0	1664976	4	US-09-916-421B-1	Sequence 1, Appli
16	40.2	0.9	657	4	US-09-134-000C-865	Sequence 865, App	
17	40	0.9	1581	4	US-09-601-198-80	Sequence 80, Appli	
C	18	39.4	0.9	15016	4	US-09-601-198-60	Sequence 60, Appli
	19	38.8	0.9	1327	4	US-08-950-758-9	Sequence 9, Appli
C	20	38.8	0.9	3981	2	US-08-955-138-2	Sequence 2, Appli
21	38.6	0.9	1579	4	US-09-071-035-83	Sequence 83, Appli	
22	38.6	0.9	1680	4	US-09-071-035-81	Sequence 81, Appli	
23	38.2	0.9	3027	4	US-09-328-352-3277	Sequence 3277, Ap	
C	24	38.2	0.9	640881	4	US-09-790-988-1	Sequence 1, Appli
	25	38	0.9	399	4	US-09-621-976-8976	Sequence 8976, App
26	38	0.9	30549	4	US-09-134-001C-322	Sequence 322, App	
C	27	37.8	0.9	474	4	US-09-621-976-18033	Sequence 18033, A

RESULT 1

```

US-09-833-381-1810
; Sequence 1810, Application US/09833381
; Patent No. 6672186
; GENERAL INFORMATION:
; APPLICANT: Robison, Keith E.
; TITLE OF INVENTION: No. 6672186el Nucleic
; FILE REFERENCE: 5800-119
; CURRENT APPLICATION NUMBER: US/09/833,381
; CURRENT FILING DATE: 2001-04-11
; PRIOR APPLICATION NUMBER: 09/515,448
; PRIOR FILING DATE: 2000-02-29
; NUMBER OF SEQ ID NOS: 2050
; SOFTWARE: Fast-SEQ for Windows Version 3.0
; SEQ ID NO 1810
; LENGTH: 3033
; TYPE: DNA
; ORGANISM: Homo sapiens
US-09-833-381-1810

```

Query Match

Query Match	60.3%;	Score 2584.6;	DB 4;	Length 3033;
Best Local Similarity	98.0%;	Prod. No. 0;		
Matches 2648;	Conservative	0; Mismatches 4;	Indels 51;	Gaps 1;
1636	GTCTAAAANTCCCTGTTTCAGCTTGT	TTTTAAAAATAGATAAAGCTATATATCGAGTAAA	1695	
6	GTCCGAAAAATTCCTGTTTCAGCTTGT	TTTTAAAAATAGATAAAGCTATATATCGAGTAAA	65	
1696	GTGAAAGCTGAAACCATCTGAGAAAGTCTCTCTTAGGATCTCTGTGACACAGCCTGACTCC	1755		
66	GTGAAAGCTGAACCATCTGAGAAAGTCTCTCTTAGGATCTCTGTGACACAGCCTGACTCC	125		
1756	ATAGTTGGGATTGTAGCTGTTTGACAAAGTGTGAATCTGATGAATGCCTCTAAATGATATT	1815		
126	ATAGTTGGGATTGTAGCTGTTTGACAAAGTGTGAATCTGATGAATGCCTCTAAATGATATT	185		
1816	ACAATGGAANAATGTGGTCCATGAGTTGGAACTTTTATACACAGAAATATATTATAGGCAATG	1875		
186	ACAATGGAANAATGTGGTCCATGAGTTGGAACTTTTATACACAGGATATATTATAGGCAATG	245		
1876	TTCATGAATCTTTTGGAGTCTTTTCAGGAATGTGGACTCTGGGTATTGACAGATGCAAAAC	1935		
246	TTCATGAATCTTTTGGAGTCTTTTCAGGAATGTGGACTCTGGGTATTGACAGATGCAAAAC	305		
1936	CTCAGCAAGGATTATATTGATGGTGTATTATGACAATGCAGAAATATGCTGAGAGGTTTTATG	1995		
306	CTCAGCAAGGATTATATTGATGGTGTATTATGACAATGCAGAAATATGCTGAGAGGTTTTATG	365		
1996	GAGGAAAAATGAAGGACATATTGTAGATATTCATGACTTTTCTTTGGGTAGCAGTCCACAT	2055		

Db	366	GAGGAAAATGAAGGACATA	TGTAGATATT	CTATGAC	CTTTCTTTGGGTACGAGTCCACAT	425
Qy	2056	GTCCGAAAGCATTTTCCAGAGACT	TGGATT	TGGGTAGACACCAACATGGGTTACAGGATT	2115	
Db	426	GTCCGAAAGCATTTTCCAGAGACT	TGGATT	TGGGTAGACACCAACATGGGTTACAGGATT	485	
Qy	2116	TACCAAGAAATTTGAAGTAACT	GTACCTGATT	CTATCACTTCTTTGGGTGGCTACTGGTTT	2175	
Db	486	TACCAAGAAATTTGAAGTAACT	GTACCTGATT	CTATCACTTCTTTGGGTGGCTACTGGTTT	545	
Qy	2176	GTGATCTCTGAGGACCTGGGTCT	TGGACTAA	CAACTACTCCAGTGGAGCTCCCAAGCCTTC	2235	
Db	546	GTGATCTCTGAGGACCTGGGTCT	TGGACTAA	CAACTACTCCAGTGGAGCTCCCAAGCCTTC	605	
Qy	2236	CAACCATTTTTCATTTTTTTTGAAT	CTTTCCCTA	CTCTGTTATCAGAGGTGAAGAAATTTGCT	2295	
Db	606	CAACCATTTTTCATTTTTTTTGAAT	CTTTCCCTA	CTCTGTTATCAGAGGTGAAGAAATTTGCT	665	
Qy	2296	TTGGAAATAACTATATTCAATATT	TTTTCGAAAGTCCCACTGAGGT	TAAAGTAAATCAATTGAG	2355	
Db	666	TTGGAAATAACTATATTCAATATT	TTTTCGAAAGTCCCACTGAGGT	TAAAGTAAATCAATTGAG	725	
Qy	2356	AAAAGTGACAAATTTTGATATT	TCTAATGACTTCAAGTGAAT	TAAATGCCACAGGCCACCAAG	2415	
Db	726	AAAAGTGACAAATTTTGATATT	TCTAATGACTTCAATGAAAT	TAAATGCCACAGGCCACCAAG	785	
Qy	2416	CAGACCCCTCTGGTCCGAGTGAGGAT	TGGGCACTGTTCTTTTCCCATCGGCCAACA	2475		
Db	786	CAGACCCCTCTGGTCCGAGTGAGGAT	TGGGCACTGTTCTTTTCCCATCGGCCAACA	845		
Qy	2476	CATCTGGAGAAATTCCTATCACA	GCTCACAAGCTTTTCA	CCCCACTGTTCTGATGCTGTC	2535	
Db	846	CATCTGGAGAAATTCCTATCACA	GCTCACAAGCTTTTCA	CCCCACTGTTCTGATGCTATC	905	
Qy	2536	ACCAGATGATTTTGTAGTAAAGGCT	GTGAAGGAATAGAAAAATCATATT	CACAATCCATCTTTA	2595	
Db	906	ACCAGATGATTTTGTAGTAAAGGCT	GTGAAGGAATAGAAAAATCATATT	CACAATCCATCTTTA	965	
Qy	2596	TTAGACTTGACTGCAATAGAGCT	ACAGGTACCCCTGAAAACTTTTGAGTTTCTCATTTTCC	2655		
Db	966	TTAGACTTGACTGCAATAGAGCT	ACAGGTACCCCTGAAAACTTTTGAGTTTCTCATTTTCC	1025		
Qy	2656	CCTAATACAGTGACTGGCAGTGAAAGAGT	TCAGATCACTGCAATGGAGATGTTCTTGCT	2715		
Db	1026	CCTAATACAGTGACTGGCAGTGAAAGAGT	TCAGATCACTGCAATGGAGATGTTCTTGCT	1085		
Qy	2716	CCITCCATCAATGCTTAGCTCATTCAT	TCGGATGCTTATGCTGTGGTGAACAGAAC	2775		
Db	1086	CCITCCATCAATGCTTAGCTCATTCAT	TCGGATGCTTATGCTGTGGTGAACAGAAC	1145		
Qy	2776	ATGATAAATTTTGTCTCCAAATATT	TATGATTTTGGATTATCTGACTAAAAAGAACCACTG	2835		
Db	1146	ATGATAAATTTTGTCTCCAAATATT	TATGATTTTGGATTATCTGACTAAAAAGAACCACTG	1205		
Qy	2836	ACAGATAATTTTGAAGAAAAAGCTCT	TATATGAGGCAAGGTTACACAGAGAACTT	2895		
Db	1206	ACAGATAATTTTGAAGAAAAAGCTCT	TATATGAGGCAAGGTTACACAGAGAACTT	1265		
Qy	2896	CTCTATCAGAGGGAAGATGGCTCT	TTTTCAGTGCTTTTGGGAATTATGACCCCTCTGGGAGC	2955		
Db	1266	CTCTATCAGAGGGAAGATGGCTCT	TTTTCAGTGCTTTTGGGAATTATGACCCCTCTGGGAGC	1325		
Qy	2956	ACTTGGTTGTGAGCTTTTGTTTTAA	GATGTTTCCCTGAAAGCCGATCCTTACATAGATATT	3015		
Db	1326	ACTTGGTTGTGAGCTTTTGTTTTAA	GATGTTTCCCTGAAAGCCGATCCTTACATAGATATT	1385		
Qy	3016	GATCAGAAATGTTTACACAGAAACAT	ACATCTGGCTTAAAGGACATCAGAAATCCACCGT	3075		
Db	1386	GATCAGAAATGTTTACACAGAAACAT	ACATCTGGCTTAAAGGACATCAGAAATCCACCGT	1445		
Qy	3076	GAAATTTTGGGATCCAGGGAAGTGA	TTTATAGTGAGCTTTCAAGGTGGCAATAAAGTCCA	3135		
Db	1446	GAAATTTTGGGATCCAGGGAAGTGA	TTTATAGTGAGCTTTCAAGGTGGCAATAAAGTCCA	1505		

2845 ACTGCCACCAATATGCTAGAGAAATCTCCCGAGCTTCTGCTCAGTTTGGGAGACAT 2904
 2709 TCTGTGCTCTCCATCAATAGGCTTAGCCTCAITGATTCGGATGCCCTTATGCTGTGGTGA 2768
 2905 ATTAGGCTCTGCCATGCAAAACACACAAATCTCTCCAGATGCCCTATGCTGTGGAGA 2964
 2769 ACAGACATGATATAATTTGCTCCAAATATTTACATTTTGGATATCTGACTAAAAAGAA 2828
 2965 GCAGATATGCTCTCTTCTGCTCCTAACATCTATGACTGATTTATCTAAATGAACACA 3024
 2829 ACAACTGACAGATAATTTGAAGAAAAAGCTTTTCATTTATGAGGCAAGGTTTACAGAG 2888
 3025 GCAGCTTATCTCCAGAGATCAAGTCCAGGCCATGGCTATCTCAACACTGGTTTACAGAG 3084
 2889 AGAAGCTTCTCTATCAGAGGAAGATGGCTTTTTCAGTGTCTTTTGGG-----AATTATGA 2942
 3085 ACAGTTGAACACTACAAACACTATGATGGCTCTACAGCACCTTTTGGGGAGCGATATGGCAG 3144
 2943 CCCTTCTGGGAGCACTGGTGTGCTTGTGCTTTTGAAGATGTTTCTTGAAGCCGATCC 3002
 3145 GAACAGGGGCAACACCTGGCTCAGCCTTTGTTCTGMAAGACTTTTGGCCAGCTCGAGC 3204
 3003 TTACATAGATATTTGATCAGAAATGTGTACACAGAACATACACTTGGCTTTAAAGGACATCA 3062
 3205 CTACATCTTCTATCGATGAAGCACACATTACCCAGGCCCTCATATGGCTCTCCAGAGGCA 3264
 3063 GAATCCAAAGGTAATTTGGGATCCAGAGAGTATTCATAGTAGGCTTCAAGGTGG 3122
 3265 GAAGGCAATAGGCTTTTTCAGAGCTCTGGGTCACTGCTCAACATGCCATAAAGGAGG 3324
 3123 CAATAAAGTCCAGTAACTTACAGCTATATTTGAATCTTCTCTCTGGGATATAGAAA 3182
 3325 AGTAGAAGATGAAGTGAACCTCTCCGCTATATCACCATGCCCTTCTGGAGATCTCTCT 3384
 3183 GTATCAGCTTAACTTGAATGGAAGTCTATCCATTTTGGAGTCTGAATTCAGTAG 3242
 3385 CACAGTCACTCACCTTGTGTCGCAATGCCCTGTTTGGCTGGAGTCAAGCTTGAAGAC 3444
 3243 AGGA 3246
 3445 AGCA 3448

RESULT 4
 US-09-566-921-109
 ; Sequence 109, Application US/09566921
 ; Patent No. 668288
 ; GENERAL INFORMATION:
 ; APPLICANT: Loring, Jeanne F.
 ; APPLICANT: Tingley, Debra W.
 ; APPLICANT: Edwards, Carla M.
 ; TITLE OF INVENTION: GENES EXPRESSED IN ALZHEIMER'S DISEASE
 ; FILE REFERENCE: PA-0024 US
 ; CURRENT APPLICATION NUMBER: US/09/566,921
 ; CURRENT FILING DATE: 2000-05-05
 ; NUMBER OF SEQ ID NOS: 138
 ; SOFTWARE: PERL Program
 ; SEQ ID NO 109
 ; LENGTH: 4792
 ; TYPE: DNA
 ; ORGANISM: Homo sapiens
 ; NAME/KEY: misc feature
 ; OTHER INFORMATION: Incyte ID No. 668288 369213.15
 US-09-566-921-109

Query Match 2.5%; Score 108.4; DB 4; Length 4792;
 Best Local Similarity 50.0%; Pred. No. 1.2e-20;
 Matches 302; Conservative 0; Mismatches 296; Indels 6; Gaps 1;
 2649 ATTTCTCTCTAATACAGTGAAGTGAAGAGTTCAGATCACTCAATTCGAGATGT 2708
 3041 ACTGCCACCAATATGCTAGAGAAATCTGCCGAGCTTCTGCTCAGTTTGGGAGACAT 3100

2709 TCTGTGCTCTCCATCAATAGGCTTAGCCTCAITGATTCGGATGCCCTTATGCTGTGGTGA 2768
 3101 ATTAGGCTCTGCCATGCAAAACACACAAATCTCTCCAGATGCCCTATGCTGTGGAGA 3160
 2769 ACAGACATGATATAATTTGCTCCAAATATTTACATTTTGGATATCTGACTAAAAAGAA 2828
 3161 GCAGATATGCTCTCTTCTGCTCCTAACATCTATGACTGATTTATCTAAATGAACACA 3220
 2829 ACAACTGACAGATAATTTGAAGAAAAAGCTTTTCATTTATGAGGCAAGGTTTACAGAG 2888
 3221 GCAGCTTCTCTCCAGAGATCAAGTCCAGGCCATGGCTATCTCAACACTGGTTTACAGAG 3280
 2889 AGAAGCTTCTCTATCAGAGGAAGATGGCTTTTTCAGTGTCTTTTGGG-----AATTATGA 2942
 3281 ACAGTTGAACACTACAAACACTATGATGGCTCTACAGCACCTTTTGGGGAGCGATATGGCAG 3340
 2943 CCCTTCTGGGAGCACTGGTGTGCTTGTGCTTTTGAAGATGTTTCTTGAAGCCGATCC 3002
 3341 GAACAGGGGCAACACCTGGCTCAGCCTTTGTTCTGMAAGACTTTTGGCCAGCTCGAGC 3400
 3003 TTACATAGATATTTGATCAGAAATGTGTACACAGAACATACACTTGGCTTTAAAGGACATCA 3062
 3401 CTACATCTTCTATCGATGAAGCACACATTACCCAGGCCCTCATATGGCTCTCCAGAGGCA 3460
 3063 GAATCCAAAGGTAATTTGGGATCCAGAGAGTATTCATAGTAGGCTTCAAGGTGG 3122
 3461 GAAGGCAATAGGCTTTTTCAGAGCTCTGGGTCACTGCTCAACATGCCATAAAGGAGG 3520
 3123 CAATAAAGTCCAGTAACTTTCAGAGCTATATTTGAATCTTCTCTCTGGGATATAGAAA 3182
 3521 AGTAGAAGATGAAGTGAACCTCTCCGCTATATCACCATGCCCTTCTGGAGATCTCTCT 3580
 3183 GTATCAGCTTAACTTGAATGGAAGTCTATCCATTTTGGAGTCTGAATTCAGTAG 3242
 3581 CACAGTCACTCACCTTGTGTCGCAATGCCCTGTTTGGCTGGAGTCAAGCTTGAAGAC 3640
 3243 AGGA 3246
 3641 AGCA 3644

RESULT 5
 US-09-621-976-2813
 ; Sequence 2813, Application US/09621976
 ; Patent No. 6639063
 ; GENERAL INFORMATION:
 ; APPLICANT: Dumas Milne Edwards, J.B.
 ; APPLICANT: Jobert, S.
 ; APPLICANT: Giordano, J.Y.
 ; TITLE OF INVENTION: ESTs and Encoded Human Proteins.
 ; FILE REFERENCE: GENSET.054PR2
 ; CURRENT APPLICATION NUMBER: US/09/621,976
 ; CURRENT FILING DATE: 2000-07-21
 ; NUMBER OF SEQ ID NOS: 19335
 ; SOFTWARE: Patent.pm
 ; SEQ ID NO 2813
 ; LENGTH: 832
 ; TYPE: DNA
 ; ORGANISM: Homo sapiens
 ; NAME/KEY: CDS
 ; LOCATION: 235..399
 US-09-621-976-2813

Query Match 1.1%; Score 49; DB 4; Length 832;
 Best Local Similarity 9.5%; Pred. No. 0.00076;
 Matches 34; Conservative 175; Mismatches 150; Indels 0; Gaps 0;
 2830 CAACGTGACAGATAATTTGAAAGAAAAAGCTCTTTTCATTTATCAGGCAAGGTTTACCAGAGA 2889
 1 YRWYWKYTTWYAKCWTGKWSWSYWKYWKYWKYWKYWKYWKYWKYWKYWKYWKYWKYWKYWKYWKY 60

Query Match 1.1%; Score 47.4; DB 1; Length 7218;
Best Local Similarity 4.5%; Pred.No. 0.01;
Matches 18; Conservative 217; Mismatches 168; Indels 0; Gaps 0

RESULT 8
US-08-447-411-1
; Sequence 1, Application US/08447411

Best Local Similarity 63.0%; Pred. No. 0.011;
Matches 68; Conservative 0; Mismatches 40; Indels 0; Gaps 0;
QY 3481 GGAATCCCAATATGAGTGGCTTAACGAGGCAAGAAATAGTTCGGTGGTTTTCATCT 3540
Db 19 GCAACCAACATCGTGAAGTGGATCAGAGCAGCAGAAATGCCAGGCGGTTTCTCCTCC 78
QY 3541 ACTCAGGATACCACTGTGGCTTTAAAGGCTCTGTGAAATTTGCAGCC 3588
Db 79 ACCAGGACACAGTGGTGGCTCTCCATGCTCTGTCCAAATATGGAGCC 126

RESULT 11
US-09-241-606-3
; Sequence 3, Application US/09241606
; Patent No. 6472140
; GENERAL INFORMATION:
; APPLICANT: Tanzi, Rudolph E.
; APPLICANT: Kovacs, Dora
; APPLICANT: Saunders, Aleister J.
; TITLE OF INVENTION: Alpha-2-Macroglobulin Therapies and Drug Screening Methods for
; TITLE OF INVENTION: Alzheimer's Disease
; FILE REFERENCE: 0609.4460003
; CURRENT APPLICATION NUMBER: US/09/241,606
; CURRENT FILING DATE: 1999-02-02
; NUMBER OF SEQ ID NOS: 27
; SOFTWARE: Patentin Ver. 2.0
; SEQ ID NO 3
; LENGTH: 750
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: CDS
; LOCATION: (1)..(750)
; OTHER INFORMATION: A /LRP Binding Domain
US-09-241-606-3

Query Match 1.0%; Score 44; DB 4; Length 750;
Best Local Similarity 63.0%; Pred. No. 0.02;
Matches 68; Conservative 0; Mismatches 40; Indels 0; Gaps 0;
QY 3481 GGAATCCCAATATGAGTGGCTTAACGAGGCAAGAAATAGTTCGGTGGTTTTCATCT 3540
Db 19 GCAACCAACATCGTGAAGTGGATCAGAGCAGCAGAAATGCCAGGCGGTTTCTCCTCC 78
QY 3541 ACTCAGGATACCACTGTGGCTTTAAAGGCTCTGTGAAATTTGCAGCC 3588
Db 79 ACCAGGACACAGTGGTGGCTCTCCATGCTCTGTCCAAATATGGAGCC 126

RESULT 12
US-09-621-976-2813/c
; Sequence 2813, Application US/09621976
; Patent No. 6639063
; GENERAL INFORMATION:
; APPLICANT: Dumas Milne Edwards, J.B.
; APPLICANT: Jobert, S.
; APPLICANT: Giordano, J.Y.
; TITLE OF INVENTION: ESTs and Encoded Human Proteins.
; FILE REFERENCE: GENSET.054PR2
; CURRENT APPLICATION NUMBER: US/09/621,976
; CURRENT FILING DATE: 2000-07-21
; NUMBER OF SEQ ID NOS: 19335
; SOFTWARE: Patent.pm
; SEQ ID NO 2813
; LENGTH: 832
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: CDS
; LOCATION: 235..399
US-09-621-976-2813

Query Match 1.0%; Score 42.8; DB 4; Length 832;
Best Local Similarity 12.2%; Pred. No. 0.049;
Matches 47; Conservative 166; Mismatches 173; Indels 0; Gaps 0;
QY 954 TGGACCAAGTGAATTTTAAACCAAGTGAAGCAAGATCAGTTACAGGTATTTCAAGAAATGT 1013
Db 387 TGTACCAATAAATATATATTTTGTYYTWTWTKWYTTTWTWMMKKKARRWYWWK 328
QY 1014 AAGCACTAAATGTGTCTTCAAGCAACATGATTACATCATTTGAGTTTTCATTATATAC 1073
Db 327 STYACASRYRYKYTWGWWYWKMMSTRWYCYWCKWCCMYRGRCAWYTWARGMWSYAW 268
QY 1074 TGTCTTGAAGCCATCTCTCAACTTCAGCCACTGTGAAGTAACTCGTCTGCTGATGCCAA 1133
Db 267 GKXSMESASMCRTMYKKGSTYWTMKCTCATCYWYWKYWKMMSKTCSGSRGGYMT 208
QY 1134 CCAACTGACTCTTGAAGAAAGAAATAATAGTAGTCATACAGTGAACAGACAGAGAACTA 1193
Db 207 SYSTRSYMTWASWYTMCMWGRWWSYTWYWANGKKWRYATTWRRATWYWAATMM 148
QY 1194 TACTGAGTACTGGAGCGGATCTAACAGTGGAAATCAGAAAATGGAAGCTGTTTCAGAAA 1253
Db 147 WYMWKAMCSSLRGAAMYRRITMMWGYRYWKKSYRTRCAWAYAWTKRKYWCMRWKW 88
QY 1254 AAATTATCTGTCCTCCCAAGAGTGAACCTTTTAAAGTGAATTCCTCAATCTCGGAGGATTC 1313
Db 87 KRCMMWMMMAAYGKTMWRACWKTRYRWMAWMMWMTMMMMYWYWRAMKRRWNR 28
QY 1314 CAGTGAGCTACAGTTGAAGGCTATT 1339
Db 27 KWRSSWYMWANGMTWRWARMWY 2

RESULT 13
US-10-204-708-2/c
; Sequence 2, Application US/10204708
; Patent No. 6577731
; GENERAL INFORMATION:
; APPLICANT: OLEK, Alexander
; APPLICANT: PIEPENBROCK, Christian
; APPLICANT: BERLIN, Kurt
; TITLE OF INVENTION: Diagnosis of Diseases Associated with DNA Replication
; TITLE OF INVENTION: by Assessing DNA Methylation
; FILE REFERENCE: 5013.1012
; CURRENT APPLICATION NUMBER: US/10/204,708
; CURRENT FILING DATE: 2003-05-06
; PRIOR APPLICATION NUMBER: PCT/EP01/03971
; PRIOR FILING DATE: 2001-04-06
; PRIOR APPLICATION NUMBER: DE 10019058.8
; PRIOR FILING DATE: 2000-04-06
; PRIOR APPLICATION NUMBER: DE 10019173.8
; PRIOR FILING DATE: 2000-04-07
; PRIOR APPLICATION NUMBER: DE 10032529.7
; PRIOR FILING DATE: 2000-06-30
; PRIOR APPLICATION NUMBER: DE 10043826.1
; PRIOR FILING DATE: 2000-09-01
; NUMBER OF SEQ ID NOS: 98
; SEQ ID NO 2
; LENGTH: 10467
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: chemically treated genomic DNA (Homo sapiens)
US-10-204-708-2

Query Match 1.0%; Score 41.6; DB 4; Length 10467;
Best Local Similarity 46.4%; Pred. No. 0.67;
Matches 169; Conservative 0; Mismatches 194; Indels 1; Gaps 1;
QY 813 ATCCTTTTGGGGAAGAGAAAATATTACAAAAACATTTTAAAGATAATGATCTGCAAA 872
Db 8823 ATTCTATTAAATAACCAATATATTAAATAAAAAAAAAAAAAAAAAAAACATAACAAA 8764

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QY      873  CTCTCTTTTAATGATGAAGAGATGAAAAATGTAATGGATTCTTCAATGGACTTTCTGA 932
Db      8763 ATAATCTATCAATCAAAAAAATAATAATAATAATAATAATAATAATAATAATAATAATAAT 8704

QY      933  ATACCTGGATCTATCTTCCCTCGGACAGTAGAAAATTTTAAACACAGTGCAGAAATCAAT 992
Db      8703 ATATCTTTATCTATTTTCTTACTACTATAACAAAATACCTAAAACTAAATAAATTTATAATA 8644

QY      993  TAGAGGTATTTCAAGAAATGTAAGCACTAATGTCTTCAAGCAACATGATTACATCAT 1052
Db      8643 AACAAAATTTATACACACAAATTTCTAAAACTAAAAATCCAAATTTAAAAATCAA 8585

QY      1053 TGAGTTTTTGAATATATCTACTGTTCTTGAAGCCATCTCTCAACTCCACGCCACTGTGAA 1112
Db      8584 CATCTTTTAAAAACCTTCTTCTCCATCATCCATAATAATAAAAAATAAAAAACAAAAA 8525

QY      1113 GGTAACTCGTCTGATGGCAACCACTGACTCTTGAAGAGAGAGAAATAATGTAGTCAT 1172
Db      8524 AAACAAAAATAAACTTACAACCTCAAACTCTTTTAATAATTAACATTATTCCAATCAT 8465

QY      1173  AACA 1176
Db      8464  AAAA 8461

RESULT 14
US-09-356-952-11
; Sequence 11, Application US/09356952
; Patent No. 6117663
; GENERAL INFORMATION:
; APPLICANT: Botiaek-Sjodin, Ann
; APPLICANT: Margalit, S. M.
; APPLICANT: Bor-Segi, Dafna
; APPLICANT: Cole, Philip
; APPLICANT: Kuriyan, John
; TITLE OF INVENTION: A CRYSTAL OF A RAS-SOS COMPLEX AND METHODS OF USE
; FILE REFERENCE: 600-1-228N
; CURRENT APPLICATION NUMBER: US/09/356,952
; CURRENT FILING DATE: 1999-07-19
; EARLIER APPLICATION NUMBER: 60/093,631
; EARLIER FILING DATE: 1998-07-21
; NUMBER OF SEQ ID NOS: 14
; SOFTWARE: Patent in Ver. 2.0
; SEQ ID NO 11
; LENGTH: 5398
; TYPE: DNA
; ORGANISM: Saccharomyces cerevisiae
US-09-356-952-11

Query Match      1.0%; Score 41.4; DB 3; Length 5398;
Best Local Similarity 47.2%; Pred. No. 0.48;
Matches 126; Conservative 0; Mismatches 141; Indels 0; Gaps 0;

QY      802  TTTTACCTTTTACCTTTTGGGAAAGAGAAAAATATTACAAAACATTTAAGATAAAT 861
Db      2671 TTTTACCTTTTCAACCGTCTCTCTCATACAGAACCTTTTCAAGAGACAGAGTTTCAAAA 2730

QY      862  GGATCTGCAAACTCTCTTTTAAATGATGAAGAGATGAAAAATGTAAATGATTCCTCAAT 921
Db      2731 AGGAAGAAAAAATATCCATTAACCTGTAGACACTTTTGAATACAAATGAAGAAGAAATCCTCG 2790

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; APPLICANT: Bult et al.
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; Patent No. 6503729
; FILE REFERENCE: PB275
; CURRENT APPLICATION NUMBER: US/08/916,421B
; CURRENT FILING DATE: 1997-08-22
; PRIOR APPLICATION NUMBER: US 60/024,428
; PRIOR FILING DATE: 1996-08-22
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Search completed: August 18, 2004, 00:43:10
Job time : 288 secs

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